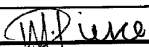


## EXPRESS MAIL CERTIFICATE

I hereby certify that this paper or fee is being deposited with the United States Postal Service "Express Mail Post Office to Addressee" service under 37 C.F.R. § 1.10 on the date indicated below and is addressed to the Assistant Commissioner for Patents, Washington, D.C. 20231.

Typed or Printed Name	Margaret Pierce	Express Mail No.	EL 563 388 228 US
Signature		Date	December 29, 2000

**NOTIFICATION  
OF PRIOR  
SEQUENCE LISTING**

Address to:  
Assistant Commissioner for Patents  
Washington, D.C. 20231

Attorney Docket	IRVN-007CON2
First Named Inventor	Gatanaga, et al.
Application Number	Unassigned
Filing Date	Herewith (December 29, 2000)
Group Art Unit	Unassigned
Examiner Name	Unassigned
Title	"FACTORS AFFECTING TUMOR NECROSIS FACTOR RECEPTOR RELEASING ENZYME ACTIVITY"

Sir:

The above-identified patent application contains sequences of nucleic acid and polypeptides. A sequence listing was prepared for the parent application, Application No. PCT/US99/10793, filed May 14, 1999, in paper and computer-readable format. The sequences in the present application are identical to those presented in the parent application. Therefore, please transfer to this application, in accordance with 37 CFR §1.821(e), the computer readable copy from applicants' other application.

As required by 37 CFR §1.821(f), the information in the hard copy and computer readable form are identical. I hereby state that this submission, filed in accordance with 37 CFR §1.821(g), does not contain new material. Applicants respectfully submit that the present patent application is now in compliance with 37 CFR §§1.821-1.825.

The Commissioner is hereby authorized to charge any fees which may be required by this paper, or to credit any overpayment, to Deposit Account No. 50-0815.

Respectfully submitted,  
BOZICEVIC, FIELD & FRANCIS LLP

Date: December 29, 2000

By: 

Carol L. Francis  
Registration No. 36,513

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Facsimile: (650) 327-3231  
F:\DOCUMENT\IRVN (UC Irvine)\007con2\notice of prior seqlist.wpd

## SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Gatanaga, T.  
Granger, G.A.
- (ii) TITLE OF INVENTION: Factors Altering Tumor Necrosis  
Factor Receptor Releasing Enzyme Activity
- (iii) NUMBER OF SEQUENCES: 154

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: MORRISON & FOERSTER  
(B) STREET: 755 PAGE MILL ROAD  
(C) CITY: Palo Alto  
(D) STATE: CA  
(E) COUNTRY: USA  
(F) ZIP: 94304-1018

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: Windows  
(D) SOFTWARE: FastSEQ for Windows Version 2.0b

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: USSN 09/081,385  
(B) FILING DATE: 014-NOV-1998

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME:  
(B) REGISTRATION NUMBER:  
(C) REFERENCE/DOCKET NUMBER: 22000-20577.21

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 650-813-5600  
(B) TELEFAX: 650-494-0792  
(C) TELEX: 706141

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4047 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAGCTTTTTC	CTTTCCTTCC	CCGGGAAAGG	CGGGGCCAG	AGACCCGCAC	TCGGACCAGG	60
CGGGGGCTGC	GGGGCCAGAG	TGGGCTGGGG	AGGGCTGGGA	GGGCGTCTGG	GGCCGGCTCC	120
TCCAGGCTBG	GGGCCGCCAG	CTCCGGGAAG	GCAGTCTTGG	CCTGCGGATG	GGGCCGCGCG	180
TGGGGCCCGG	CGGGCGGGCC	TGGGGAGGCG	TCCAGGCTGC	GGGAGCGGGA	GGAGCGGCGG	240
TGCGGGCGCC	AGCGCCCTGG	GTGGAGGTGC	CCGTCCCTCC	TGAGGGGCGA	CCAGTGCCTT	300
TGGGACCCGG	GAGCAGAGCC	CGCGCTCTCC	CAGCGGCTTC	CCCGGGGGTC	TCACCGGGTC	360
ACCCGAGAGC	GGAGGCCCGG	GCTCCGCAGA	AACCCGGGGC	GGCCGCGGGG	AAGCAGCGCC	420
CTCAGGCGTC	GGAGGAGGCC	CCAGAAAGAC	CTCGGCGCTT	CCC GCCGGG	TCCGACCGCC	480
TGGGTTCCGT	GGGGGACGGC	CCAGGCCGCC	AGGACCCCCA	AGCGCAGCTC	AGTCTGCGGG	540
GCACGACCCA	GAGGCCAGCA	GCAGAGGACG	GGGCCGGGGC	CGGGAGAGGG	CGGGGAGGGC	600
GCTCCTGGGA	GGTCAAGGCC	AGGGCTAGAC	TTTCAGGCTC	ATGGCTGGCC	CCCTCATCCC	660
CAGGGAGGTG	AGGGGGCTCT	GTGAGCAGAG	GGGGCCCGGG	TGGAGAGAGC	GCTGCTAGCC	720

AGGGCGGGGG CAGGAGCCCA GGTGGGGACT TAAGGGTGGC TGAAGGGACC CTCAGGCTGC 780  
 AGGGATAGGG AGGGAAGCTA GGGGTGTGGC TTGGGGAGGT GCTGGGGGAC CGCGGGGCCC 840  
 CTTTATTCTG AAGCGGAATG TGCTGCCGAC GTCCCCAGTG ACCTAGAAAT CCAATTCAAG 900  
 ATTTTCAGGA GTTTTCAGTG GAGACAAAGG CCAGGCCAGG GTGAAATGT GGCAGTGACA 960  
 GAGTATGGGG TGAGAACACC GGAGAGAGGA AGTCCCAGAG GCGGATGATG GGACAGAGAG 1020  
 CGGGGACCAG AATTTTAA AACCACATCT AGATGCGTTT GGCAGACTCA TAGTGTGTTT 1080  
 CTTTTCAGGG AGAAAGTGTG GGCAGAGGCC AGCTCTAAAG CCCAGGCTGC CCAGCTTGCA 1140  
 TTGGCAGAGC TGACGGAAGG CCAGGGCAGA GCCTTCCCTC CCTGTACAG ACATGAGGCC 1200  
 TGGAGATCTG GAATGAGGCA GATGTGCCCA GGGAAAGCTG ATCCGCCCCG ACCCAGGGCC 1260  
 CCCCAGGTCG CCTTTGAGC GTGGAACTGT TGCCAGGTCA TGGCTCCCTG CTATCGAGAA 1320  
 CGGGACACGG GTGCTGTGCT GCACC TGGA GATTGACAGC CGACACCCAC AATGCTTAA 1380  
 GAGTGATGA CTGCTTTCCA GGGGCTGGC TGCTGACAC TTTGATGGC TCCTGGAGAA 1440  
 GAGGGATTGA GTGGAGTCCA CGGGCTATGG CACGCTCCTG GGTGCTGCT CTGAGGCAGG 1500  
 GCCTCGCTGG GGTGAGAAGG GGCTGGAGC AGGTTCTGTC CAGTTCAGCC TCTAACCGGT 1560  
 GGTCTTCATG CTTAGGAACC CACTGGGGGG TTATGAAACT GCAGGTGGCT GAGTCTTTCG 1620  
 CATGGGTCTC CTCCTTCAGG AGGTCTGGT GGGGCCGGAG ACTGTACCCC ACAAGAGGTC 1680  
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 CTGGCGCCCA GGGCCTGGGC TTGAGACAGC TGTCAGCAGC GCAAGCCATT TACCCCGTTT 1800  
 TTGGGGACAT TACATCTTCC TAGCTTGGAA CACACAGGCA GCCAGGTTTG TTATCCACAT 1860  
 TCCTCTCTCA TGTTCTTCTC TTGAGAACTT TTACCGGTA TGTCAAGAGG TGGCTCCAC 1920  
 CAGGGAGACT CAAGTGGAAA GCGCTCATCC TTGTCTCTCA GGAGACAGGA AAACCTATGG 1980  
 TTACAATTCC AGGGACAAGA GCGATGTCAT TGAGGTGTGG CAAATCTCAC TGTTCACTG 2040  
 GAGAAATCAG AGAAGCCTTC CTGGAGGCGA TGACACCTGG ACAGGCTTCT CCACAGGAGG 2100  
 AAGCGAGTGA GAGAAGCCAA CTGGGATGGA CCGCATGATG AGGGGGAACA GTGCGCGAGG 2160  
 AACCAACAAC CACCCCCACC CTAGGCCGAG AGCTCACGGA GAGAGCTGGG CCTCTCGGGG 2220  
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 TGCTATTTTC CACACCAGAA ATCATATCTC CTTGCTGGTC CATGTCTGAA GACCTTACAC 2580  
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 AAACCTTATT ACTATGTATG TTTCTCAAAC CACCTGCAAC AATGGGACTT GATACCGATG 3060  
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 ACATCATCAT TCCACTTTGT ACATATCTGT TCTGATGCT TTTCTCCCTG AAAACATTAG 3360  
 GACTCCTTGC CAGGACGGCC TGCAACAAGA CTGGTATGTC ACCTTCTGGG TCATCACTGC 3420  
 CAAGGTTATC TTTCACTCT ATGTGATCTG TTGATACCTG GTTGAGGCTA TGGACAGCT 3480  
 CTGAAACCAA ATTGTCTACC CTACAAGCCA AAAGGCAGTT CACCTCTTCT GCTATTCTGT 3540  
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 TCAGGAGGTC TGTGAGACTA GCAATCCCCG CAAGAGTAGT AATGGGGACA TGGGGCATAT 3660  
 CCCCATTCACT CTGAATTTCT TGAATGGTGT TTGCTATAA AAGTACTTAG TTCAAGTGCC 3720  
 AGCTGTCAAT ACTTCCCAT TCCCAAACAC TGGGCGAATC GCGCTCTGAA TCCAAGGGGA 3780  
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 CAAATCTGTT CTCTTCTTCT CTCTCTCTCC TCTTCTCTCC ACATAGAAAC ACTCACAAC 3960  
 ACCAGCCAC GGGCCCGAGC TACCGGGGGG GCATCGCCGC GGGCCCGGGA ACCAATTCTC 4020  
 CTGTGCGCGG GGGCCTCCTT TGGATCC 4047

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 739 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGATCCAAAG GTCAAACTCC CCACCTGGCA CTGTCCCCGG AGCGGGTCGC GCCCGGCCGG 60  
 CGCGCGCGCC GGGCCTTGGC GCCAGAAAGC AGAGCCCTC GGGCTCGCC CCCCAGCTC 120  
 ACCGGGTACG TGA AAAAACG ATCAGAGTAG TGGTATTCA CCGCGGCCCC GAGAGGCCGG 180  
 CGGACCCCGC CCGGGGCCCT TCGCGGGGAC ACCGGGGGGG CCGCGGGGCG CTCCCACTTA 240

TTCACACCT	CTCATGTCTC	TTCACCGTGC	CAGACTAGAG	TCAAGCTCAA	CAGGGTCTTC	300
TTTCCCCTG	GATTCGCCA	AGCCCGTTCC	CTTGGCTGTG	GTTTCGCTGG	ATAGTAGGTA	360
GGGACAGTG	GAATCTCGT	CATCCATTCA	TGCGGCTCAC	TAATTAGATG	ACGAGGCATT	420
TGGCTACCTT	AAGAGAGTCA	TAGTACTCC	CGCCGTTTAC	CCGCGCTTCA	TTGAATTCTC	480
TCACTTTGAC	ATTGAGAGCA	CTGGGCAGAA	ATCAGATCGC	GTCACACCCC	CGCCGCGGCC	540
TTCCGAGTGC	TTTGTTTTAA	TAAACAGTC	GGATTCCCTT	GGTCCGCACC	AGTCTCTAAG	600
CGGCTGCTAG	CGCCGCGCCG	AAGCAGAGCG	CGCGCGGAA	CGCGGCCCC	CGGGCGGAC	660
CGCGGGGGG	GACCGGCGG	CGGCCCTCC	GCCCGCTGCC	GCCGCGCGCG	CGCGCGCGCG	720
CCGAGAGAGA	AGGGGGGAAA					739

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CAAGAGTGGC	GGCCGACGCA	GGCCCCCGGG	GTGCCCCGGC	CCCCCTCGAG	GGGGACAGTG	60
CCCCCGCCGC	GGGGGCCCCG	CGCGCGGGCG	CGCGCGGGCC	CTGCGCGCCC	GACCCCTTCTC	120
CCCCCGCCGC	CGCCCCCAGC	CGCGCTCTCC	CGGGGAGGGG	GGGAGGACGG	GGAGCGGGGG	180
AGAGAGAGAG	AGAGAGAGGG	CGCGGGGTGG	CTCGTGCCGA	ATTCAAAGAG	CTT	233

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGATCCAAAG	AATTCGGCAC	GAGGTAGTCA	CGGCTCTTGT	CATTGTTGTA	CTTGACGTTG	60
AGGCTGGTGA	GCTTGGAAAA	GTGATGCGC	AGCGTGCAGC	AGGCGTTGTA	GATGTTCTCG	120
CCGTCACGCG	ACAGCTTGGC	GTGCTGGCGC	CTCAGCGGGT	CCGCATACCT	CAGCAGGGCC	180
TGGAACCTGG	TGTTCTTGGT	GAAGGTGATG	ATCTTCAACA	CTGTGCCGAA	CTTGAGAGAA	240
ATCTGTGTGA	GCACATCCAG	GGTCACAGGG	TAGAAGAGGT	TCTCCACGAT	GATCCTGAGC	300
ACGGGGCTCT	GCCCCGCCAT	CGCCATCCCT	GCATCCACGG	CGCGCCGCCA	GGCAGCCAAAG	360
GCCAGGTTCC	CGCACTGGAC	CGAGTTCACC	GCCTGCAGGG	CGCGCTGGGG	CGCGCCCTGG	420
TTGGGAGAGC	TGTCGGTCTT	CAGCTCCTTG	TGGTTGGAGA	ACTGGATGTA	GATGGGCTGG	480
CGCGCAGGCA	CAGGGGTCAC	CGAGGTGTAG	TAGTTCACCA	TGGATTATGG	AGCCTCCTCC	540
GTGTTATCT	CGATGAAGGC	CTGGTTTTTC	CCCTTCAGCA	TCAGGAGGTT	GGTGACCTTC	600
CCAAAGGGCA	GGCCAGGGGA	GATGACTTCC	CCCTCCGTGA	CGTCGATGGG	GAGCTTCCGG	660
ATGTGGATCA	CTCTAGAGGG	GACGCTGCA	CTTCGGCTGT	CACCTTTGAA	CTTCTTGTCT	720
TCATTTCCGT	TTGCTGCAGA	AGCCGAGTTG	CTGCTCATGA	TAAACGGTCC	GTTAGTGACA	780
CAAGTAGAGA	AAAGCTCGTC	AGATCCCCCG	TTTGTACCAA	CGGCTATATC	TGGGACAACT	840
CCGTCATAGG	CACACAGAGC	AGACCCGCGG	GGGACGGAGT	GGAGGCGCGG	GAATCCTGGA	900
GCTAGAGCTG	CAGATTGAGT	TGCTGCGTGA	GACGAAGCGC	AAGTATGAGA	GTGCTCTGCA	960
GCTGGGCCCC	GGCACTGACG	CCCACTCTTA	CAGCCTGCTG	CAGACCCAGC	ATGCACTGGG	1020
TGATGCCCTT	GCTGACCTCA	GCCAGAAGTC	CCGAGAGCTT	CAGGAGGAAT	TTGGCTACAA	1080
TGCAGAGACA	CAGAAACTAC	TATGCAAGAA	TGGGGAACCG	CTGCTAGGAG	CCGTGAACCT	1140
CTTTGCTCTT	AGCATCAACA	CATTGGTCA	CAAGACCATG	GAAGACACGC	TCATGACTGT	1200
GAACACGAT	GAGGCTGCCA	GGCTGGGAAT	TGATGCCTAC	CGAAGACACT	TAGAGGAGCT	1260
GAGTCTAGGC	CCCCGGGATG	CAGGGACACG	TGGTCGACTT	GAGAGTGCCC	AGGCCACTTT	1320
CCAGGCCCAT	CGGGACAAGT	ATGAGAAGCT	GCGGGGAGAT	GTGGCCATCA	AGCTCAAGTT	1380
CTTGGAGAAA	AAACAAGATCA	AGGTGATGCA	CAAGCAGCTG	CTGCTCTTCC	ACAACTGCTGT	1440
CGCTGCCCTAC	TTTGCTGGGA	ACCGAAGAAC	GCTGGAGCAG	ACCTTCGAGC	AGTTCAACAT	1500
TAAGCTGGGG	CTCCAGGAG	CTGAGAAGCC	CTCCTGGGTA	GAGGAGCAGT	GAGTCGCTCC	1560
CAGGCCAACT	TGGCTATCAA	GAAGACATT	GGGAAGGGCA	GCCCCAGGTT	GTGGGAGATT	1620
GGACATGGTA	TCCTTTTGT	CATTGCCCT	CTGGCTTGGG	CTCCTTTTTC	GAGCTGGGGG	1680
CTGACCAACG	TTTTGCCCAT	ATTGCTATGG	TGGGAAGAGG	GCCTGGAGGC	CCAGAAAGTTG	1740
CTGCGCTGTC	TATCTTCTGT	GCCACAGGGC	TTCAATCCCA	GATCTTTTCC	TTCCACTTCA	1800
CAGGCAACGG	CTATGACAAA	ACCACTCCCT	GGCCAAATGG	ATCACTCTTC	AGGCTGGGGT	1860
GAGCTCCCTG	ACCAATGACA	GAGCCTGAAT	ATGCCCTGTC	AGCCAATGGC	AGCTCTTCTC	1920
GAGCTCCCTT	GGGCCAATGA	TGTTGCTCT	AATACCTTTT	GTCTCTCTTC	TATGCTGACC	1980
CATTGCAGAG	AAGGGGACTG	GGACAAAGG	GGTGGGGATA	ATGGGGAGCC	CCATTGCTGG	2040

CCTGCACTCT	GAATAGGCCT	ACCCTCACCA	TTTATTCAC	AATACATTTT	ATTGTGTTT	2100
TCTAATTTAA	AATTACCTTT	TCATCTTGCT	TGATTTTCT	TCAGCTAAAT	TAGAAATTTG	2160
TAGTTTTTTC	CCTAAAAAAT	TCAATGGCAT	TCITTTCTAT	AAATACATT	CTCTGATTTT	2220
CTGTGCAGCC	TGCTCAAGG	AAATCCATGT	GTTCAAAATG	CTTGCTCGCA	GTTTGTCTCA	2280
TACCAAATGG	TGCTTAACC	CAATATCTG	AGCAGCAAT	TGAGCTGATC	CTTCTGGAGA	2340
AAGTAGCGTT	GAACAGCCAA	GACCACTGG	TAGTCGAAGA	GAAGACCACA	CATCCTGAAC	2400
TCCCAAGTCT	GGTGTAGGG	GAGGACAGCT	GATAACTGGA	TATGCAGTGT	TCCAGACAT	2460
CACGTGTCCC	AAACCATTAC	TTCTGCCTGC	CACCTGCCAC	AATACAGTAG	GAATGCCATC	2520
CCCTTCATAC	TCAGCTTTAA	TCTCAGAGT	TTTATCTGTT	CCTTTATGCG	CAGATGTTAC	2580
TCGAAGTTCA	CATGGAATGC	CAAAATTTCC	ACAGGCCCTC	TTGATTTTTT	CACAGTGACC	2640
AAGATCAGAA	GTAGAGCCCA	TCAACACTAC	AACCTGCAC	TGACTTTCTG	ATTTCAAAGG	2700
CAACTCTACT	CTCTCTGCAA	CCCACCTCAA	GTITTTCTTT	ACCATTGGA	GCCCTTCAGG	2760
AGTTACTTCT	TTGAGGTCCC	GATAAGACTG	TTTGTCTTTC	TGTTGGCTTC	GATCTCTGTA	2820
TGGCCAGAGT	CTCCAGGAAT	CATTGTCAAT	AACATCAGCA	AGAACAATTT	CTTTGGTGGT	2880
TACATCACAA	CCAAATTCAA	TCTTCTATCT	AACCACTGTA	CAATTCTGGG	GCAACCAAGG	2940
TTTCTCCAGT	ATTTCAAATA	TAGCCTGTGT	AGCATCTCGT	GCCGAATTC	AAAAGCTT	2998

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AAGCTTTTGG	TGAAAAACCT	AGGATATGTC	CCCTCCCTCA	CCACACCCAA	CCCCCCCCCC	60
CTGCCCCAGG	ACATGACATG	GCCTCACACA	CACACACACA	CACACATACA	CACAAGGCCG	120
TGAGCTGCAC	CGAGGAACAT	GGGCTGCAC	CACGACAACA	TTGAAAAAAT	ATACATTATA	180
TATGTACACC	CGGGGCCCCC	ACGTCCCCCT	CCGTCCCCGC	AGCCTGGCCA	CACCAAGGTCA	240
CGGAGGAGGG	CGCGGGGCTG	CAGGACCTCA	GGACTGCAAG	GGCAGGAAGG	GAACAGGAGC	300
AAGAAAGGAA	GGAAGTTGGA	AAGGAGGGAG	AAATGGGGTC	CCAGACTGGA	AATGGAAATG	360
AGGTGGGGCG	ATCATAAGAG	AAGCAGGGAC	GATGGTCCAG	CTGAGGGAGC	CCTGCAGAGG	420
GGGAAAAGCT	TCCCATGGAC	AGGAGAGAGA	AGGGAAGGGG	AGAGGAGAGG	GTTTCTTCA	480
ATCCCCACCC	CAGGCCCAAG	CCGACCCCCA	GCCATTGCAA	TGCTCACCCT	CTCCCCAACA	540
CAGTGAAGTC	TAAAGGGGGA	GCTGCCATTG	GGGGTAGAAA	GGCAGCTGAA	GTCCAGGCCA	600
CTTTCCAAACC	CAGCCAGCCC	CAGTGCAAGG	GGCACAACAG	GAGCATGACA	GCCCCAGAAT	660
GAGGATGGTG	GGGGCCGGGG	AGGGGCAGGG	CGGACTCCAG	AGGGCCCCGT	GGGGTTTTGA	720
AATGAAAGGA	GGACTGGTTC	TGAAGCCTCT	CTCCCTCTTG	GTCTCTGTGT	TCCAGAAAGG	780
TGGGGGAATC	ATGTCTGGAG	TGCTGTGTTT	ACCAAGGCAG	AATTCCTCCT	CTGCGTGGGG	840
AGAGGTGTAG	GCCTTAGTAG	CGGTGTGGGG	GGGTGTGAT	GATGCTCTCT	TGCTGCTGCT	900
TGGGGGAATC	GGCCACCTCC	GAGTCACTGC	TGTCTCTATC	CTCCTGCTGG	CCCCCAACAG	960
CCCCCGTCAC	ACAGGACTGC	CGATTCTGGT	AGGACTCCAT	GGGGTTCACA	ATGATGGTGA	1020
GAGCTGAGTC	ATCCCAAGAG	AGGTCTGGGT	CCTTGGGGTC	ACTGGAGGCC	CCTGGAGGCT	1080
CGCCGGCCCC	TGAGACGCGG	CGGTGAAGGG	AATGGATGCG	CACCAGGCCCC	AGGACGACCA	1140
TGAGCACCAAG	GAAGCCACAG	CACACCAACA	TGATGAGGGT	TGCGGCGCTG	GGTATCATGG	1200
AGTTTCTGTG	GGAGCTGGCT	AGGCTGTGTC	CAGCCATCTC	AGGCGGGGGC	TGGTGACCA	1260
GGTGCAAGAA	CTGCTGGGAG	CTGAGCACTG	GGCTGGGGTG	GGCAACCCGG	TTCTATGCTG	1320
CGAGGACATT	GACCTCCAGC	ATGAATTCAT	TGCTGGAGTA	ACGGCCATTG	ATTTCCGAGT	1380
AGGAAAGGCC	GAAGTTCTGT	GTGTAGAGGG	CAGCTCCGTG	TGCGAGCCGA	TAACGAGCCT	1440
CGCTCAGGAT	CTCTTCATAC	ACAGTGATGC	TCTCCACCCC	AGCAATAGTG	AGGTAGGCA	1500
ATGTTGTGTT	GAGCTCCAGC	CCCGCTGTCT	GCAGAGAGGT	TGTTGCCAGG	AGCAGGCTTT	1560
CCCGCTCGGG	ATCCAGGTCA	TCCCCACCA	GAGAAATTTT	ACAGCCATCC	AGGTTGTGCA	1620
CAATCTCATC	CGACTGCGGT	GTGTCTGTCA	CTGTGCCCTG	CCAACTCTCA	TCCTTTTTGG	1680
CTCCACCTGT	GTGAGAAATG	GAGCAGGTGA	TTTGAAGTAC	AGGGAACAAA	GGGACGCCGT	1740
TGGTCCCTTC	AAAGTCCACA	GCTGGGCGGG	CAAAATGAGC	AGTGCCACTC	AGCAGGATCT	1800
GGGGGGGCTC	AGGCTGAAGG	ACGACCACTG	AGCCCTCCAC	TTCAGGGATG	GAGACGACAG	1860
ACTCTTGGCT	GAAGCACTTG	ACAGCAGTGG	TGAGGCGCAG	GGGCTGACG	CCGGGGCTGG	1920
CAAGGCGCAG	AGTGTTCATG	TAAAGCACAT	GCTGCAGGGC	ATGTTTGAAG	GTCTCCACAT	1980
CAATCCCCCT	CAGGGTGAGC	AGGGACTGTG	AGGGGTTTCA	GTGACCTTTC	ATGCCTTTTG	2040
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CCTGCGGGCT	CTCAGGCGGA	CCTGAGCGCA	CGCTGAAACC	AGCCAGAGTG	CCATGGAAGT	2160
AGTGTGGGAT	CGACAAAGGG	TCTCCTTGGG	TGGTGTCTGT	ACTGTTGTCT	CCCTTTTCTT	2220
TCTCTTTGTT	CTTCTCTCTA	GTCCAGCAGG	CCCCAATCAT	GAGAGCAGGC	CCCTTCTGGG	2280
TGGGTTGGAT	GAGGCCATTG	TCATGGATGA	GGGCGAGGTC	GAGGAGATGT	CCGTCGGTAT	2340
AGAGTTGTAC	TGAGGGGAAC	TCGAGGTTCA	GAGCGTAGTG	GTGCCACTCA	TCATCACAGA	2400
CTGCTCCAG	CTTCCAGAGG	AACTTGACTG	GGCGGCACT	CTCAAGCAGG	GGCCAGTAGA	2460
GGAAAGGCAAT	CTACAGCCCG	TGGACAGTCA	GCAGTAGTGA	AGAGAGCCGC	TCCTCATCTT	2520
GGACAGTGT	ACATAACGATG	GTTCCTCTTT	CCCTCTTGGC	CTTGTGGGGA	GTTACGCCAT	2580
GCTTCATCCA	GAAGCAGCAG	GTGAAGTGGT	CAGTGAAGCT	GTCTTGGGGC	CCAGAGCCCA	2640

GCCCACTGGG	GCCACCCAGG	GGCACCTGCA	CAGCCTGGGT	GCCATTGAAC	CAGTAGATCA	2700
GGCTGCTGTC	CTGGCTGTAG	TGCACCGAGA	GTCTGCTGT	CCAGTTGGCA	TGGGGCCACG	2760
GCATGGGCAA	CAGATCCACT	TCCCCACTGG	CAGCACCACA	GAGTTTCCGC	AGCGCCCGCT	2820
CTGAGTAGTT	GTACACGGTCA	CAGCCCTTGG	CCACATGGCT	GGTCTGCAGC	TCTATGGTGG	2880
CCTGAATGTT	CCAGAGTGGT	TCATCACAGG	TCTCCAGGCG	GATACCAGGG	AACAAAGCCA	2940
AGCTCCCAAG	ACCTGGTGCA	TATTCGATCC	TTTGTTTCCA	GCCTTGGCAG	CTGGGTTTAC	3000
AGGTGGGCTT	CACCTGAATC	TCCACCTCAG	CATCATCTGC	TGCCCGCTTC	TTCACCAAGT	3060
CATAAGCTGT	CACGTGTAAC	TATAGAGGCC	TCTCACCAC	GTACTGCAGC	TTCTCTGTGT	3120
TCTCAATGTT	CCCGTCATTG	TCAATGAGGA	AAGGGGTGTT	GGGTGTGAGA	ATCTCATAGT	3180
AGCAGATCTG	GCTGTACTGG	GGGGAGCAGT	ACCCTGCAAT	GGCTTCCACC	CGCAGGATGC	3240
GATCGTACAG	CTTCCCTCT	GTCCACAGCG	CACGATACAG	CCGTTCACAC	AACACTGGGG	3300
CAAACTCGTT	CACATCGTTG	ACCCGCACAT	GCACAGTGGC	CTTGTGGGAC	TTCTTGGTGT	3360
TGGCCCGCTC	GGGGCCCTCG	CCACAGTCAT	AGGCCCTGGAT	GGTGAAGGTG	TGTTCTTCTC	3420
GGGCCCTCGA	GTCCACAGGC	TCCTTGGCCC	GGATCAGCCC	CTCTCTGTGC	GCCTTGTCAA	3480
GGATCACAGC	CTCAAAGGGC	ACCCACAGCC	CATGGAGCCG	GAAGCCGCGA	ATCTCACCTG	3540
CATAGCCGAG	CGGGGCATCC	TTGTCCAAGG	CAAAGAGTGG	TGGATTCAAT	AGGACCGTGT	3600
TGTCATTCTC	CATGACGATG	CCCTGGTACT	CTGCCCTCAAT	CCATGGCTTG	TGCTTGTGTG	3660
CTTTGTTACA	GGAGCAGGAC	GCGGACAGAG	AGGCCAGCAG	AAGGGGCAGC	AGCAGGAGGG	3720
TCATGGTGGC	GGCTGGGGCA	GGGCAGGGCC	AGGCGTTTGC	CTCCCTTGGG	AGCCTCCAGG	3780
CTGGCGATTCT	CACCTTGC GG	GAGGGATACA	GGGGGGGAAA	ACCAAAATAA	AACCTCAAAAT	3840
AAATTGTGTA	GGAGGAGTCC	AGCTTAGGAC	CGGGCCAGAG	CCAGGCCAGG	CTCGGCGAAG	3900
GGGCCCTCTGC	AGGTTAGAG	GATCACTGCT	GCACCCAGCG	CCACCTTGGG	AGCCAATGAT	3960
TTTGCCATGC	CCTTGATTGC	AACAGCTGCC	TCTCTGTCTA	TGCGACAGAC	CACCTGTCTC	4020
AGGATCTCTT	CTCCACAGTC	GTACTTCTGC	TCAATCTCCT	TGCCAAGGTC	TCCTCAGGG	4080
AGACGAAGGT	CCTCTCGTAC	CTCCCCGCTG	TCCTGGAGCA	GTGATAGGTA	CCCATCTGTG	4140
ATCTTTGGAT	CC					4152

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGATCCAAAG	ATTCCGCACG	AGTGGCCACA	TCATGAACCT	CCAGGCCCCAG	CCCAAGGCTC	60
AGAACCAAGG	GAAGCGTTGC	CTCTTTGGGG	GCCAGGAACC	AGCTTCCCAAG	GAGCAGCCGCC	120
CTCCCCCTGCA	GCCGCCCCAG	CAGTCCATCA	GAGTGAAGGA	GGAGCAGTAC	CTCGGCGACC	180
AGGGTCCAGG	AGGGGCAGTC	TCCACCTCTC	AGCCTGTGGA	ACTGCCCCCT	CCTAGCAGCC	240
TGGCCCTGCT	GAACTCTGTG	GTGTATGGGC	CTGAGCGGAC	CTCAGCAGCC	ATGCTGTCCC	300
AGCAGGTGCG	CTCAGTAAAG	TGGCCCAACT	CTGTGATGCG	TCCAGGGCGGG	GGCCCGGAGC	360
GTGGAGGAGG	TGGGGGTGTC	AGTGACAGCA	GCTGGCAGCA	GCAGCCAGCG	CAGCCTCCAC	420
CCCATTTAAG	ATGGAAGTGC	CACAGTCTGT	CCCTCTACAG	TGCAACCAAG	GGGAGCCCGC	480
ATCCTGGAGT	GGGAGTCCCG	ACTTACTATA	ACCACCCTGA	GGCACTGAAG	CGGGAGAAAG	540
CGGGGGGCCC	ACAGCTGGAC	GCCTATGTGC	GACCAATGAT	GCACACAGAAG	GTGCAGCTGG	600
AGGTAGGGGG	CGCCCAAGCA	CCCTGGAATT	CTTTCCACGC	AGCCCAAGAAA	CCCCCAAGCT	660
AGTCACTGCC	CCTGCAACCC	TTCCAGCTGG	CATTCCGCCA	CCAGGTGAAC	CGGCAAGTCT	720
TCCGGCAGGG	CCCACCGCCC	CCAAACCCGG	TGGCTGCCTT	CCCTCCACAG	AAGCAGCGCG	780
AGCAGCAGCA	ACCACAGCAG	CAGCAGCAGC	AGCAGCAGGC	AGCCCTACCC	CAGATGCGCG	840
CTTTTGAGAA	CTTCTATTCC	ATGCCACAGC	AACCTTCGCA	GCAACCCCAAG	GACTTTGGCC	900
TGACGCCAAG	TGGGCCACTG	GGACAGTCCC	ACCTTGCTCA	CCACAGCATG	GCACCTTACC	960
CCCTCCCCCC	CAACCCAGAT	ATGAACCCAG	AACCTGCGCA	GGCCCTTCTG	CAGGACTACG	1020
CCCGGAGGCC	AGCGCTACCT	CAGGTCAGTA	TCCCTTTCCT	CCGCCGCTCC	CGCCGCTCTC	1080
CTAAGGAGGG	TATCCTGCCT	CCCAGCGCCC	TGGATGGGGC	TGGCACCAGC	CCTGGGAGCC	1140
AGGCCACTGG	CAACCTGTTT	CTACATCACT	GGCCCTTGCA	GCAGCCGCGA	CCTGGCTCCC	1200
TGGGGCAGCC	CCATCTCGAA	GCTCTGGGAT	TCCCGCTGGA	GCTGAGGGAG	TGCGAGTCACT	1260
TGCTGTATGG	GGAGAGACTA	GCACCCAAAT	GCCGGGAGCG	AGAGGCTCCT	GCCATGAGGAC	1320
GCAGGAGAGG	CATGAGGGCA	GTGACACAG	GGGACTGTGG	GCAGGTGCTA	CGGGCGGGAG	1380
TGATCCAGAG	CACGCGACGG	AGGCGCCGGG	CATCCCAAGG	GGCCAAATTT	CTGACCCCTG	1440
CCCAAGAGGG	TGTGGAGCTG	GCCTCACTGC	AGAATGCAAA	GGATGGCAGT	GGTTCTGAAAG	1500
AGAGCGGGAA	AAGTGTATTG	GCCTCAACTA	CCAAGTGTGG	GGTGGAGTTT	TCTGATGAGG	1560
CCTTAGCCAC	CAAGCGAGCA	CGAGAAGACA	GTGGGATGGT	ACCCCTCATC	ATCCAGGTGT	1620
CGTGCTGTGT	GGCAACTGTG	GACCCAAGT	AGGCAGCCCA	GGCTGGAGGT	CTTGATGAGG	1680
ACGGGAAGGG	TCTTGAACAG	AACCTTGCTG	AGCACAAGCC	ATCAGTCATC	GTCAACCTGCA	1740
GGCGGTCCAC	CCGAATCCCT	GGGACAGATG	CTCAAGCTCA	GGCGGAGGAC	ATGAATGTCA	1800
ATGTGGGAGG	GGAGCCTTCC	GTGGGGAAGC	CAAGCAGCGC	GGCCAGGCCC	GAGCCCTCTA	1860
CGTCCCCCAC	CAAGGCGGGC	ACTTTTATCG	CCCTCCCGGT	CTACTCCAAC	ATCACCCCAT	1920
ACCAGAGCCA	CTGCGCTCT	CCCGTGCGCC	TAGCTGACCA	CCCTCTGAG	CGGAGCTTTG	1980
AGCTACCTCC	CTACAGCGCG	CCCCCATCC	TAGCCCTGT	GGGGGAAGGC	TCTGCTCTCT	2040

ACTTCAATGC	CATCATATCA	ACCAGCACCA	TCCCTGCCCC	TCCTCCCATC	ACGCCCTAAGA	2100
GTGCCCATCG	CACGCTGCTC	CGGACTAACA	GTGCTGAAGT	AACCCCGCCT	GTCTCTCTTG	2160
TGATGGGGGA	GGCCACCCCA	GTGAGCATCG	AGGCCACGGAT	CACCGTGGGC	TCCGGTTTCC	2220
AGGCAGAAAT	CCCTTGTAGT	AGGGACCGTG	CCCTGGCAGC	TGCAGATCCC	CACAAGGCTG	2280
ACTTGTGTGT	GCAGCCATGG	GAGGACCTAG	AGAGCAGCCG	GGAGAAAGCA	AGGCAAGTGG	2340
AAGACTGCT	GACAGCCGCC	TGCTCCAGCA	TTTTCCCTGG	TGCTGGCAC	AACCAAGGCT	2400
TGGCCCTGCA	CTGTCTGCAC	GAATCCAGAG	GAGACATCCT	GGAAACGCTG	AATAAGCTGC	2460
TGCTGAAGAA	GCCCTTGGCG	CCCCACAACC	ATCCGCTGGC	AACCTATCAC	TACACAGGCT	2520
CTGACCAGTG	GAAAGTGCCC	GAGGGAAGCG	TGTTCAACAA	AGGCATTGCC	ATCTCAAGA	2580
AGGATTTCTT	CCTGGTGCA	AAGCTGATCC	AGACCAAGAC	CGTGGCCAG	TGCGTGGAGT	2640
TCTACTACAC	CTACAAGAA	CAGGTGAAAA	TGGGCCCA	TGGACTCTA	ACCTTTGGGG	2700
ATGTGATAC	GAGCGATGAG	AAGTCGCCCC	AGGAAGAGGT	TGAAGTGAT	ATTAAGACTT	2760
CCCAAAAGTT	CCCAAGGGTG	CCTCTTCCCA	GAAGAAGTCC	CCCAAGTGA	GAGAGGCTGG	2820
AGCCCAAGAG	GGAGGTGAAG	GAGGCCAGGA	AGGAGGGGA	GGAGAGGTG	CCAGAGATCC	2880
AAGAGAGGA	GGAGCAGGAA	GAGGGGCGAG	AGCGCAGCAG	CGGGGACGCG	CGAGTCAAG	2940
CCACGCAGAC	ACTACAGGCC	AATGAGTCGG	CCAGTGACAT	CCTCATCTCT	CGGAGGCCAG	3000
AGTCCACGC	CCCTGGGTCT	CGCGGTGCC	AGGCTTCGGA	GAAGCCAAAG	GAAGGGACAG	3060
GGAGTCCAG	AAGGGCAGTA	CCTTTTTCAG	AAAAAAACAA	AAAAAACAA	AAAGCTT	3117

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAATTCGGCA	CGAGGTCAGT	TTCTGTGGA	ACACAGAGGC	TGCCTGTCCC	ATTCAGACAA	60
CGACGGATAC	AGACCAGGCT	TGCTCTATA	GGGATCCCAA	CAGTGGATT	TGTTTAAATC	120
TTAATCCGCT	AAACAGTTCG	CAAGGATATA	ACGTCCTCTG	CATTGGGAAG	ATTTTATATG	180
TTAATGTCTG	CGGCACAATG	CCTGTCTGTG	GGACCATCCT	GGGAAACCT	GTCTCTGGCT	240
GTGAGGCAGA	AACCCAACT	GAAGAGTCA	AGAAATGGAA	GCGAGCAAGG	CCAGTCGGAA	300
GTGAGAAAG	CTCCAGCTG	TCCACAGAGG	GGCTTATCAC	TCTGACCTAC	AAAGGGCCCTC	360
CTCTGTCCAA	AGGTACCGCT	GATGCTTTTA	TGCTCCGCTT	TGTTTGAAT	GATGATGTTT	420
ACTCAGGGCC	CCTCAAATTC	CTGCATCAAG	ATATCGACTC	TGGGCAAGGG	ATCCGAAACA	480
CTTACTTTGA	TGTTGAACCC	GGGTGGCCCT	GTGTTCCCTT	TCCAGTGGAC	TGCCAAGTCA	540
CCGACCTTGG	GGGAATGAG	TACGACCTGA	CTGGCCTAAG	CACAGTCAGG	AAACCTTGG	600
CGGCTTGTGA	CACCTCTGTC	GATGGGAGAA	AGAGGACTTT	CTATTTGAGC	GTTTGCAATC	660
CTCTCCCTTA	CATTCTCGGA	TGCCAGGGCA	GCGCAGTGGG	GTCTTGCTTA	GTGTCAAGAG	720
GCAATGAGCT	GAACTGTGGT	GTGGTGACGA	TGAGTCCCCA	AGGCCGCGCG	AATGGATCTT	780
TGAGCATCAT	GATGTCAAC	GGTGACAAGT	GTGGGAACCA	CGCCTTCTCC	ACCAAGATCA	840
CGTTTGAGTG	TGCTCAGATA	TCCGGCTCAC	CAGCATTTCA	GCTTCAGGAT	GGTTGTGAGT	900
ACGTGTTTAT	CTGGAGAACT	GTGGAAGCCT	GTCCCGTTGT	CAGAGTGGA	GGGGACAAC	960
GTGAGGTGAA	AGACCCAAAG	CATGGCAACT	TGTATGACCT	GAAGCCCTGT	GGCCTCAACG	1020
ACACCATCTG	GAGCGCTGGC	GAATACACTT	ATTACTTCCG	GGTCTGTGGG	AAGCTTTCTC	1080
CACAGCTCTG	CCCCACAAGT	GACAAGTCCA	AGGTGGTCTC	CTCATGTGAG	GAAGAGCGGG	1140
AGCCACGAGG	ATTTCAACAA	GTGGCAGGTC	TCTGACTCA	GAAGCTAACT	TATGAAATG	1200
GCTTGTTAAA	AATGAACCTC	ACGGGGGGGG	ACACTTGCCA	TAAGGTTTAT	CAGCGCTCCA	1260
CGCCATCTCT	CTTCTACTGT	GACCCGCGCA	CCGAGCGGCC	AGTATTTCTA	AAGGAGCACT	1320
CAGATTGTTC	CTACTTGTTT	GAGTGGCGAA	CGCAGATATG	CTGCCACCT	TTGATCTGTA	1380
CTGAATGTTC	ATTCAAGAT	GGGGCTGGCA	ACTCTTCA	CCTCTGCTCC	CTGTCAAGGT	1440
ACAGTCAACA	CTGGGAAGCC	ATCACTTGGG	CGGGGGACCC	GGAGCACTAC	CTCATCAATG	1500
CTGTCAAGTC	TCGGGCCCGG	CAGGCTGGCA	CTGAGCCGTG	CCCTCAGAA	CGACGGCGGT	1560
GTCTGCTGGG	TGGCTCCAAG	CCGCTGAACC	TGCGCAGGGT	AAGGACGGA	CCTCAGTGG	1620
GAGATGGCAT	AATTGTCTGT	AAATACGTTG	ATGGCGACTT	ATGTCCAGAT	GGGATTCGGA	1680
AAAAGTCAAC	CACCATCCGA	TTCACTTGCA	GCGAGAGCCA	AGTGAACCTC	AGGCCCATGT	1740
TCTCAGGCG	CGTGGAGGAC	TGTGATACA	CCTTTCGCTG	GCCCAAGGCC	ACAGCCTGTC	1800
CCATGAGAG	CAACGAGCAT	GATGACTGCC	AGGTCAACAA	CCCAAGCACA	GGACACCTGT	1860
TGTATCTGAG	CTCCTTAAGT	GGCAGGCGGG	GATTACAGC	TGCTTACAGC	GAGAGGGGGT	1920
TGGTTTACAT	GAGCATCTGT	GGGAGCAATG	AAACTGCC	TCTTGGCTGT	GGGGCTGCT	1980
TGGACAGAC	CAGGATTAGC	GTGGGCAAGG	CCAACAAGAG	GCTGAGATAC	GTGGACCAAG	2040
TCTGCAAGCT	GGTGATCAAG	GATGGGTCCC	CTTGCTCCCT	CAAACTCGCG	CTGAGCTATA	2100
AGAGTGTGAT	CAGTTTCTGT	TGCAGGCTGT	AGGCCGGGCG	AACCAATAGG	CCCATGCTCA	2160
TCTCCCTGGA	CAAGCAGACA	TGCACCTCTT	CTTCTCTCTG	GCACACGCGC	CTGGCCTGCG	2220
AGCAAGCGAC	GAAATGTTCC	GTGAGGAATG	GAGCTCTAT	TGTTGACTTG	TCTCCCTTTA	2280
TTCATCGCAC	TGGTGGTTAT	GAGGCTTATG	ATGAGAGTGA	GGATGATGCC	TCCGATACCA	2340
ACCCGTATT	CTACATCAAT	ATTGTGTCAG	CACCTAAATC	CATGACGGA	GTGCCCTGTC	2400
CTGCCGAGGC	CGCTGTGTGC	AAAGTTCCTA	TGATGGTCC	CCCCATAGAT	ATCGGCCGGG	2460
TAGCAGGACC	ACCAATACTC	AATCCAATAG	CAATGAGAT	TTCATGAAT	TTTGAAGCA	2520

GTACTCCTTG	CCAGGAATTC	AGTTGTAAT	AAAAATTGAAC	CTGCTCAACA	GCTGAGGGAG	2580
ACTAGAAATG	ATGGGTCCAT	ATCCTGGTGC	ATTGTCATAC	AATTCAACA	ATGGTGCAGC	2640
TACCACGCTTG	TAATTTTATG	GGACTGCAAA	CAAGGCTTTT	TCTTGAAGCT	GAACCAGAAA	2700
CAACTTCTTA	TGTTCTTAG	GCTTTGTAAT	ATGTGCAGGA	ATATATGGAT	ACTGAGGAGG	2760
TTCAAAATTT	GGTCTCCACC	AGTTACCAAT	GCAATCGTCA	ATGACCCAGT	CTTGCAAAAT	2820
TCCATCCTGA	GCACCCAGTA	TCTCTGT CAT	TAAGCGTTT	AGTCCCTCAA	CTTCATCTTC	2880
TCCCTGGGTTA	AGTTCACCAC	CAGGTAGTTT	GAAGAAAGTT	GTTCCAGCT	GCAGCAGTAA	2940
CACATGGGGT	AGCCGGTGCT	CATGTACAAT	CAGAACCCCT	TCACAGCTC	TCCTCATTCG	3000
AAATTTATCA	AATTCCTCCC	TCAATGGCTG	AAATCTGGCT	GCAACAGAGC	TGCTCTCTTC	3060
GTAGAGGGGC	TCCTTTGTAC	CAAAAGTATA	ATTGGTAAGA	GGGTACAGGT	TGATGGTCCG	3120
CTCCAGGGTG	AGGGGCTTCG	TCTCTGGAT	GTACTTTGTT	CCGAAGTGA	TGACCCCGCC	3180
GGGCCAGCCG	GCTCGCAGC	GATTGGGCGG	TACCACAGAC	ATGCTGGCGA	GCTCCGGCCG	3240
TGACGGCGAG	CAGAAAGTGG	CAGGCGAGGT	AGACTTTCCC	CGTGGCGGAA	GCCTCGTGCC	3300
GAATTC						3306

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAATTCGGCA	CGAGAATGGA	TCAACCTCAA	CAACACGTTA	AAGCTAGACG	AAAGAAGTAA	60
TACACAGTGT	ATGAGTCTCA	CATGAAATAC	CCGGATGTAA	ATCCAAAGAA	ACAGGAAGCA	120
GATTTGGTGGT	TGCCAGGGAC	AAGGGCGGTG	GGAGGAGAAA	ATGSGAGATA	ACGGGACTTT	180
ACTTTTGAGG	TGATGAGAAT	GTTTTGGAGC	TAGATAGAA	TGGTGGTTGT	ACACCATTTG	240
GGATGTACTA	CCACTTAATT	GTTCACTTAA	AAAGTTAATT	TATGTGTAAT	GCATCTTAAT	300
TAAAAACAAG	GATAACATT	CAACTCCTGG	ACATTATCTT	TCCTTTCCAT	TGATGTACAG	360
GCCCGTGTTA	GAATTCCTCAT	CCGGTTTGGT	CACCTGCACT	AAGATGTGGA	GAATATAGGA	420
CGCACAGTTA	AGAGGAAGGA	TAACACTGAT	TAAGGTAGTG	CTTTTCTAGG	TTTCCCTCAA	480
ACAATTTAAC	AGATGGATAG	TGGCACCAC	TACAGATGAG	AAAAACCAAG	GGAAAGGAAG	540
TTTGGGGGAG	AAGTTAAGTT	TGCTTTGGGC	CTGTGTTTTG	CAACCTTGAT	GTAAAGAGCA	600
TATGTTAAGT	CTTCAGTGGC	GAACACTTAA	AAGTAAAGAT	GGATCAGAA	TTTATCTTTG	660
GATGTGACTT	CTCAAGGATG	GCTTTGTGAC	TTCACTGCC	GGTCAAATGA	CAAGATGGGC	720
AATCTTTTCC	TGAAGGTCCA	AGCACTGAA	CGTGGCAGG	TGACCCGAT	CCGATTTGCT	780
TAGAACAATC	TAGTTTCATG	CCTATTGTCC	CTCATGTAAT	TAATATCAT	CTCAAAATGT	840
CTCATTTTGT	GCAATAAATT	CTGCAACGTG	ATGGCCGACG	TCTCGCGGCC	CGAGCGGCGG	900
GACCTGTGCT	TGAGGAAGA	GGACCTCCCC	TATGAGGAGG	AAATCATGCG	GAACCAATTG	960
TCTGTCAAA	GCTGGCTTCA	CTACATCGAG	TTCAACAGG	GGCGCCCGAA	GCCCAAGGCT	1020
AATCAGCTAT	ACGAGCGGGC	ACTCAAGCTG	CTGCCCTGCA	GCTACAAAT	CTGGTACCCA	1080
TACCTGAAGG	CGCGTCGGGC	ACAGGTGAAG	CATCGCTGTG	TGACCGACCC	TGCTATGAA	1140
GATGTCAACA	ACTGTGATGA	GAGGGCCTTT	GTGTTTCATG	ACAAGATGCC	TGCTGTGTGG	1200
CTAGATTACT	GCCAGTTCC	CATGAGCCAG	GGGCGGCTCA	CACACACCCG	CCGACCTCTC	1260
GACCGTGCCC	TCCGGGCAC	GCCCATCAGG	CAGCACTCTC	GAATTTGGCC	CCTGTATCTG	1320
CGCTTCTCTG	GCTCACACCC	ACTGCCCTGAG	ACAGCTGTGC	GAGGCTATGC	GGGCTTCTCT	1380
AAGCTGAGTG	CTGAGAGTGC	AGAGGAGTAC	ATTGAGTACC	TCAAGTCAAG	TGACCGGCTG	1440
GATGAGGGCC	CCCAGCGCCT	GGCCACCGTG	GTGAACGACG	AGCGTTTCGT	GTCYAAGGCC	1500
GGCAAGTCCA	ACTACCACT	GTGGCACGAG	CTGTGCGACC	TCACTCCCCA	GAATCCGGAC	1560
AAGGTACAGT	CCCTCAATGT	GGACGCCATC	ATCCGCGGGG	GCCTCACCCG	CTTCACCGAC	1620
CAGCTGGGCA	TGCTGTGGTG	TTCTCTCGCC	GACTACTACA	TCCGACGCGG	CCATTTCGAG	1680
AAGGCTCGGG	ACGTGTACGA	GGAGGCCATC	CGGACAGTGA	TGACCGTGGC	GGACTTCACA	1740
CAGGTGTTTG	ACAGCTACGC	CCAGTTTCGAG	GAGAGCATGA	TGCTGCAAAA	GATGGAGACC	1800
GCTCGGAGC	TGGGGCCGCA	GGAGGAGGAT	GATGTGGACC	TGAGGCTGCG	CCTGGCCCCG	1860
TTCGAGCAGC	TATCAGCCG	CGGGCCCTGT	CTCCTCAACA	CGCTCTTGT	GCGCCAAAAC	1920
CCACACCACG	TGCACGAGTG	GCACAAGCGT	GTCGCCCTGC	ACGAGGCGCG	CCCCGGGGAG	1980
ATCATCAACA	CTACACAGCA	GGCTGTGCA	ACGGTGGACC	CCCTCAAGCG	CACAGGCAAG	2040
CCCCACACTC	TGTGGGTGGC	GTTTGCCAA	TTTATGAGG	ACAACGGACA	GCTGGACGAT	2100
GCCCTGTGTA	TCTTGGAGAA	GGCCACCAAG	GTGAACCTCA	AGCAGGTGGA	TGACCTTGCA	2160
AGCGTGTGGT	GTCAGTGGCG	AGAGCTGGAG	CTCCGACACG	AGAACTACGA	TGAGGCTTGT	2220
CGCTGTCTGC	GAAAGGCCAC	GGCGCTGCCT	CGCCGCGCGG	CCGAGTACTT	TGATGGTTCA	2280
GAGGCCGTGC	AGAACCAGCT	GTACAAGTCA	CTGAAGGTCT	GCTCCATGCT	CGCCGACCTG	2340
GAGGAGAGCC	TGCGACCTT	CCAGTCCACC	AGGCGCTGT	ACGACCGCAT	CTCGGACCTG	2400
CTGTATCGAA	CACCCAGAT	CGTCATCAAC	TATGCCATGT	TCTGAGAGGA	GCACAAAGTAC	2460
TTGAGAGAGA	GCTTCAAGGC	GTACGAGCGC	GGCATCTCGC	TGTTCAAGTG	GCCCCAAGCTG	2520
TCCGACATCT	GGAGCACTTA	CCTGACCAAA	TTTATGCCC	GCTATGGGGG	CCGCAAGCTG	2580
GAGCGGGCAC	GGACCTGTT	TGAACAGGCT	CTGGACGGCT	GCCTCCCAAA	ATATGCCAAG	2640
ACCTGTATAC	TGCTGTACGC	ACAGCTGGAG	GAGGAGTGGG	GCCTGGCCCG	GCATGCCATG	2700
GCCGTGTACG	AGCTGCCAC	CAGGCGCGTG	GAGCCCGGCC	AGCAGTATGA	CATGTTCAAC	2760



ATCTACATCA	AGCGGGCGGC	CGAGATCTAT	GGGGTCACCC	ACACCCGCGG	CATCTACCA	2820
AAGGCCATTG	AGGTGCTGT	GGACGAGCAC	GCGCGTGAGA	TGTGCCTGCG	GTTTGCAGAC	2880
ATGGAGTGCA	AGCTCGGGGA	GATTGACCGC	GCCCGGGCCA	TCTACAGCTT	CTGCTCCAG	2940
ATCTGTGACC	CCCGGACGAC	CGGCGCGTTC	TGGCAGACGT	GGAAGGACTT	TGAGGTCCCG	3000
CATGGCAATG	AGGACCACT	CAAGGAAATG	CTGCGTATCC	GCCGCAGCGT	GCAGGCCACG	3060
TACAACACGC	AGGTCAACTT	CATGGCCTCG	CAGATGCTCA	AGGTCTCGGG	CAGTGCACG	3120
GGCACCGTGT	CTGACCTGGC	CCCTGGGCGC	AGTGGCATGG	ACGACATGAA	GCTGCTGGAA	3180
CAGCGGGGAG	AGCAGCTGGC	GGCTGAGGCG	GAGCGTGACC	AGCCCTTGGC	C6CCCAGAGC	3240
AAGATCCTGT	TCGTGAGGAG	TGACGCCTCG	CGGAGGAGGC	TGGCAGAGCT	GGCAGCAGAG	3300
GTCAACCCCG	AGGAGATCCA	GCTGGGCGAG	GACGAGGACG	AGGACGAGAT	GGACCTGGAG	3360
CCCAACGAGG	TTGCGCTGGA	GACGACGAGC	GTGCCAGCCG	CAGTGTTTGG	GAGCCTGAAG	3420
GAAGACTGAC	CCGTCCCCCT	GTGCCGAATT	CGGCACGAGC	AAGACCAGCC	CCCAGATCAT	3480
TTGCCCTCAA	GGTTTTCCTT	CGAAGTCACA	AATGTTTCAA	GGAATCTCAA	ATTTTACAAA	3540
GTTTGAAGTG	TGGGCATTGG	TGGCCTGTGG	CTGTGTCCCT	TCTCTGTAGC	TGTTTTCTCC	3600
CTACATCCCT	GAAAGGAAGT	TGAGCTGTCT	CCTCCATCCG	CAGACCTCCC	TTTCCAGCGC	3660
CCAGGGCATG	GGTGCTGTG	AGGGCAGCAT	GCTAGGTGTG	ACCGTGCTCC	TGGCCTCCAG	3720
GCCCGTGTCC	CTCTGTCTCT	TAGCCCACTA	AGGCCCTGGC	CCATTGTGTC	TAAACAGGCCA	3780
GCTCGGACCT	GAAAGAGCAG	ACAATCTCTC	TGGGTCACCA	GTCTGGCTAG	GAGCTGGTCT	3840
CTTGACTGGG	ATCCAGGCCT	TCTCCCTGCG	CCATGTGAAT	TCCCAAGGCG	AGAGCTGAA	3900
ATGTTGAACA	CAGCAGCTGC	CAAAGAGATG	TCACCGTGGG	AACCGAGGCT	CTCTTCTCCT	3960
CTCGCTGCT	TTGCTGGGTT	CAGATAGCT	GAGGCTTGTG	TGAGAGGAGT	TGAGTGTCTG	4020
GTTTTCACCC	TGGTTGGTGT	GCTTTGGTTT	GAGGGCACTT	AGAAAGCCCA	CGCCAGGCTG	4080
TGCTCTGCTG	CTGCACACAG	CGGAGCGACT	TTTCTAGGTA	TGCTCTTGAT	TTCTGCAGAA	4140
GACGAGGTG	GCAATGGAGC	AAGAGGAAGT	GTGACTGAAA	CTGTCCACTC	ATAGCCGCGC	4200
TGCCGTATTG	AGAGGGCT					4218

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1187 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAGCTCGCGC	GCCTGCAGGT	CGACACTAGT	GGATCCAAAG	AATTCGGCAC	GAGGGAAACT	60
CAACGGTGTA	CGAGTGGAGG	ACAGGGACAG	AGCCCTCTGT	GGTGGAAACG	CCCCACCTCG	120
AGGAGCTTCC	TGAGCAGGTT	GCAGAAGATG	CGATTGACTG	GGGCGACTTT	GGGGTAGAGG	180
CAGTGTCTGA	GGGGACTGAC	TCTGGCATCT	CTGCCGAGGC	TGCTGGAATC	GACTGGGGCA	240
TCTTCCCGGA	ATCAGATTCA	AAGGATCCTG	GAGGTGATGG	GATAGACTGG	GGAGACGATG	300
CTGTTGCTTT	GCAGATCACA	GTGCTGGAAG	CAGGAAACCA	GGCTCCAGAA	GGTGTGCCA	360
GGGGCCAGGA	TGCCCTGACA	CTGCTTGAAT	ACACTGAGAC	CCGGAATCAG	TTCTTGTATG	420
AGCTCATGGA	GCTTGAGATC	TTCTTAGCCC	AGAAGAGCAG	GGAGTTGAGT	GAGGAGGCAG	480
ATGTCCTGTC	TGTGAGCCAG	TTCAGCTGGG	CTCAGCCAT	CCTGCAGGGC	CAGACCAAAG	540
AGAAGATGGT	TACCATGGTG	TCACTGCTGG	AGGATCTGAT	TGGCAAGCTT	ACCAGTCTTC	600
AGCTGCAACA	CCTGTTTATG	ATCCTGGCCT	CACCAAGGTA	TGTGGACCGA	GTGACTGAAT	660
TCTCTCAGCA	AAAGCTGAAG	CAGTCCAGCT	TGCTGGCTTT	GAAAGAAAGG	CTGATGGTGC	720
AGAAGCAGCA	GAGGGCACTT	GAGGAGCAGG	CGGCTCTGGA	GCCTAAGCTG	GACCTGCTAC	780
TGAGAGAAGC	CAAGGAGCTG	CAGAAGCTGA	TTGAAGCTGA	CATCTCCAAG	AGGTACAGCG	840
GGCGCCCTGT	GAACTGTGAT	GGAACCTCTC	TGTGACACCC	TCCGTGTTCT	TGCTGTGCCA	900
TCTTCTCCGC	TTTTGGGATG	AGATGATAG	CCAGGGCTGT	TGTTTTGGGG	CCCTTCAAGG	960
CAAAAGACCA	GGCTGACTGG	AAGATGGAAA	GCCACAGGAA	GGAAGCGGCA	CCTGATGGTG	1020
ATCTTGGCAC	TCTCCATGTT	CTCTACAAGA	AGCTGTGGTG	ATTGGCCCTG	TGCTCTATCA	1080
GGCGAAAACC	ACAGATTCTC	CTTCTAGTTA	GTATAGCGCA	AAAAGCTTCT	CGAGAGTACT	1140
TCTAGAGCGG	CCGCGGGCCC	ATCGATTTC	CACCCGGGTG	GGGTACC		1187

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCCTCACTAA	AGGGAACAAA	AGCTGGAGCT	CGCGCGCCTG	CAGGTGCACA	CTAGTGGATC	60
GAAAGTTCGT	TACGCCAAGC	TGCAAAATTA	CTCTGGGCTG	ACCCATAAAC	ATTTGTCTGA	120

TCTAGGATAT AGTTGCGTTT CTGCGGGCA GCAATCTGGA TGAGGCGGTT GAGGCACTGG 180  
GTGGCTGCT GGAATCAGGAC ATCCACGCG CCAGCATAGT TCCGCTGCCG GCGTAGGCCC 240  
ATCACCCGCA TCTTATCCAT GATGGCATTG GTACCCAGGA TGTGTACTT CTGGAAGGG 300  
TTGAGGCTG CATGTTTATG GGCCCATGTG GTCTTGCCAG CAGCAGGACG GCCCACCATC 360  
ATCAGAACTCT CACATCTCTG CTCTGCTTTT GGTCCAACGG TGCCCCGGAT ACCTCACTA 420  
AGGGGAAGGT GCTGGATGAA GGTAAACCCC GGGAGGACAG AACAGTAGGG CTCTGCTCTC 480  
TGTCGGAAGT TGAATCCAC TCGCAATTC TTACCCAGGA CATGAGGATA GAGGCGCTGA 540  
CCCCCAAGG CTTCCTTCTG GATTCGGAAA GCAATGCCCA TCCACTTTCC ATTCTTGCTA 600  
AAAGACAGTT CCACGTCATT TCCACATTCA AAATCCGCAA AGCAGGCAAT CACCGAGAG 660  
CTCTGCGGTG CTAGGAGAGC GGTGGGCC CCAGACTGGG GGGAAAGCTC CGCAGCCGCA 720  
GTGGGCCCA GGAATCAGCC CCGCTGGCC TGGAGAACC CAGTCTGGCG TGAAGCGGGA 780  
GCTGGACATG GTGGCTTGGC GTTCCGCC CCAGAGCGCTG CGAGTGTGCG GGCCTCGGGT 840  
GGATTTGCTG AGCACCATAA CCTCACGGTT GCCAACCTGG GGTTTAGCT CCCTTGGTTT 900  
TAATCCCTA GGGCGGGTG GGGCACGG AGGAAGGATG GGCAGCTGG GTGCAATCTC 960  
GCTGTAGGCC AGCATTCTCT TGAATTTCTA GAATTAAC TAACGGTCCG CCGGAGGCCG 1020  
TCGGGGCCGG AGCGAGCAG CCGCGGCTGA GGTTCGCG TCGGCCGCTC GGGGCTGCGC 1080  
TCCCGCGCCG GACCCCGCG CTCTGGCCG GCGGCTCCG GCTCCGGGG GGGCGGGG 1140  
CGCGGGGACA TGGTGCCAGT CGCACCCCTT CCGCGCCGCC GCTGAGCTCG CCGGCGCGC 1200  
CCGGGCTGGG ACCTCCGAGC GGGGAAGATG TTTCCGCC CTGAGTCCAGT GAGGAAGCTG 1260  
ACCAAGGCCCC GGGCGGGAC AAGAACATCC CCGCGGGCTG CAGTCCAGT AACCGAGGCT 1320  
TGCAAGCGCG CTTCGCCAAG GGGGTGCACT ACAACATGAA GATAGTGATC GCGGAGACA 1380  
GGAACACCGG CAGACAGCG CTGTGGCACC GCCTGCAGGG CCGCGGCTTC GTGAGGAGT 1440  
ACATCCCCAG ACAGGAGATC CAGGTCCACA GCATCCACTG GAGCTACAG AACCGAGTAT 1500  
ACATCGTGAA GGTGAGTGT TGGGATGTAG TAGACAAGG AAAATGCAAA AAGCGAGGG 1560  
ACGGCTTAA GATGGAGAAC GACCCCAAG AGNCGGAGTC TGAATGGCC CTGAGTCTG 1620  
AGTTCTCGGA CGTGTACAAG AACTGCAAG GGGTGGTCA TATGTTTCAG ATTACCAAGC 1680  
AGTGACCTT CAATTACATT CTCCGGGAGC TTCCAAAGT GCCCACCAC GTGCCAGTG 1740  
GGTGCTGGG GAATCAACGG GACATGGGCG AGCACCAGT CATCTCCG GAGCACGTG 1800  
GTGACTTCAT CGACAACCTG GACAGACCTC CAGTTCTCT CTACTTCG TATGCTGAGT 1860  
CTTCCATGAA GAACAGCTTC GGCCTAAAT ACCTTCATAA GTTCTTCAAT ATCCCATTT 1920  
TGCAGCTTCA GAGGAGACG CTGTTGCGCG AGCTGGAGAC GAACCAAGTG GACATGGAGC 1980  
CCACGCTGGA GAGCTGTGCG GTGCAGCAG AGACGGAGGA CCAGAAGTAC GGCATCTTC 2040  
TGGAGATGAT GAGGCTCGC AGCGGTGGCC ATGCTCACC ACTGGCGGCC AACGGGACA 2100  
GCCATCTCCC GGGCTCCAG TCACAGCTCC TGCTGCACC CGCTGTGTC ACGGGGAGCT 2160  
CCAGCCCGCG CACACCCAG CCGGCCAC AGCTGCCCT CAATGCTGCC CCACCATCT 2220  
CTGTGCCCCC TGTACACCC TCAAGGCCCG TGCCCCACC TGCGTGCCC TCAGCCCCG 2280  
CCCCACGGCG CAGCATCATC TCTAGGCTGT TTGGAGCTC ACCTGCCAC GAGGCGGCC 2340  
CTCACCTCC AGAGCCAGTC CCGGCCGAC AGGGCCGAC AACGGTCCAG AGTGTGGAG 2400  
ACTTTGTCTC TGACGACCGC CTGGACGCA GCTTCTGGA AGACACAACC CCGCGCAGG 2460  
ACGAGAAGAA GGTGGGGGCC AAGGCTGCC AGCAGGACAG TGACAGTAT GGGGAGGCC 2520  
TGGCGGGCAA CCGATGGTG GAGGGTTCC AGGACGATG GGACCTCGAA GACCAAGCC 2580  
GTGGAGTCC CCGCTGCC TCGAGGCCCG TCCCGAGTCA AGACATCACT CTTTCGAGT 2640  
AGGAGGAAGC AGAAGTGGCA GCTCCACAA AAGGCCGTC CCGAGCTCCC CAGCAGTGT 2700  
CAGAGCCAGA GACCAAGTGG TCTCCATAC CAGCTCGAA GCCACGGAG GGGACAGCTC 2760  
CCACAGGAC CGCAGCACCC CCTGGCCAG GCGGTGTCT TGTTCCGACA GGTCCGGAGA 2820  
AGCGACGAC CACGAGGCC CCTGTGAGA TGGAGCCGG GAAGGGTGA CAGGCTCTCT 2880  
CGTCCGAGAG TGACCCCGAG GACCCATTG CTGACAAAT GCTGTCTTC GTCATGGATG 2940  
ACCCGACTT TGAGAGCGAG GGAATCAGACA CACAGCGAG GCGGATGAC TTTCCGTCG 3000  
GAGATGACCC TCCGATGTG ACTGACGAGG ATGAGGGCC TGCCGAGCG CCCCCACCC 3060  
CCAAGCTCCC TCTCCCGCC TTCACTGTA AGAATGACT GGACCTCTC GGGCTGGGCG 3120  
TGGAGGAGC CGGACCCAG GAGAGCAGTG AGGAAGGTA GAGGGGCAA ACCCCCTCTA 3180  
AGGAGAAGAA AAAAAAACA AAAAGCTCT CGAGAGTACT TCTAGAGCG CCGCGGCC 3240  
ATCGAATTTT CACCCGGGTG GGTACCAAG TAAAGTGACC CAATTCGCC TATAGTGAGT 3300  
CGTATT

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGCGGGGCA GAGTGGGCTG

20

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCAGTCCTGG CCTGCGGATG

20

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTCGACAGGA GAATTGGTTC

20

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCCTGGGTTT GGTGCGGGAC

20

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TGGTCGGGTG TTTGTGAGTG

20

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCTCTCCGT CTCCTCAGTG

20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGATTGCTAG TCTCACAGAC

20

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTAAGGGTGG CTGAAGGGAC

20

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ACCTTCCTC CCTGTCACAG

20

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGGTCGGGTG TTTGTGAGTG

20

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ACACCATTCC AGAAATTCAG

20

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AAACTGCAGG TGGCTGAGTC

20

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTCCTAATGT TTTCAGGGAG

20

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AAAACCTATG GTTACAATTC

20

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TCCTAGACAT GGTTC AAGTG

20

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GATATAATTA GTTCTCCATC

20

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATGCCTGTC CAGGCTGCAC

20

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGACGGCGAC CTCCACCCAC

20

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGGCTCCTCC GACGCTGAG

20

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AGTCTAGCCC TGGCCTTGAC

20

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTCAC TG GGG ACTCCGGCAG

20

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CAGCTTTCCC TGGGCACATG

20

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CACAGCTGTC TCAAGCCAG

20

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

ACTGTTCCCC CTACATGATG

20

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ATCATATCCT CTTGCTGGTC

20

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GTTCACAGAG CTTGCTGTG

20

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GTTCGACAGA CTCATAGTTG

20

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TAGCAGGAG CCATGACCTG

20

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CTTGGCGCCA GAAGCGAGAG

20

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CCTCTCTCTC TCTCTCTCTC

20

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TCCCCGCTGA TTCCGCCAAG

20

(2) INFORMATION FOR SEQ ID NO:42:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CTTTTGAAT TCGGCACGAG

20

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CCCCTGGTCC GCACCAATTG

20

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GAGAAGGGTC GGGCGGCAG

20

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

AAATCACATC GCGTCAACAC

20

(2) INFORMATION FOR SEQ ID NO:46:



- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TAAGAGATC ATAGTTACTC

20

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GCTCTAGAAG TACTCTCGAG

20

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ACTCTGCCA TCAGGAGATC

20

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CAGGCGTTGT AGATGTTCTG

20

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AGTGGCAGGC AGAAGTAATG

20

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:  
GGTTGGAGAA CTGGATGTAG 20

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:  
CTATTGAGAT GCAACGCCAG 20

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:  
CCATGGCACA CAGAGCAGAC 20

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:  
GCTACCATGC AGAGACACAG 20

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:  
CAGGCTGACA AGAAATCAG 20

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:  
GGCACGCATA GAGGAGAGAC 20

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

TGGGTGATGC CTTTGCTGAC

20

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

AAAACAAGAT CAAGGTGATG

20

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TTGCCCATG TGCTATGGTG

20

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GACCAAGATC AGAAGTAGAG

20

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CCCCTGGGCC AATGATGTTG

20

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

TCTTCCACC ATAGCAATG

19

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TGGTCTGGT GACCAATGTG

20

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACACCTCGGT GACCCCTGTG

20

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TCTCCAAGTT CGGCACAGTG

20

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ACATGGGCTG CACTCAGCAC

20

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GATCCTCTGA ACCTGCAGAG

20

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GGAAATGAGG TGGGCGCATC 20

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CTTGCCTTG GACAAGGATG 20

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GCACCTGCCA TTGGGGGTAG 20

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GGTGGAAGCC ATTGACGGTG 20

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TGCGTCTCTC GTCGCTGCTG 20

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GCGGAACTC TGTGGTCTG 20

(2) INFORMATION FOR SEQ ID NO:74:

- (1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

AGGATTGCCT TCCTCTACTG

20

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

TGCTGTTC ACCAGGGCAG

20

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

CCAGTGCCTC TATGCATGTC

20

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

AGGAAGCCCA CGCACACCAC

20

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CCCTTTGTC CCTGATCTTC

20

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CGCTCGGGAT CCAGGTCATC

20

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TCGAGGTTCA GAGCGTAGTG

20

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TCTTGGATCT CTGGCACCTC

20

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CCATCAGAGT GAAGGAGGAG

20

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

CCATCTTCCA CTGGTCAGAG

20

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CTCCTTCTCT TGGATCTCTG

20

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TTACTTCAGC ACTGTTAGTC

20

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

AGGGAGGTAG CTCAAAGCTC

20

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

TGGGTCCACA GTTCGCACAG

20

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CAACTCTGTG ATGGCTCCAG

20

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

AGCAGGGTTC TGTCAAGAC

20

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CCATTGGGTG CTAGTCTCTC

20



(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

CAGCCATGCT GTCCAGCAG

20

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CTGGACCTGA GGTAGCGCTG

20

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ATAACCACCC TGAGGCACTG

20

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CCTGCAGGTC GACACTAGTG

20

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

AATTGGAATG AGGAGGACTG

20

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:  
GCTCTAGAAG TACTCTCGAG 20

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:  
ATTGTATGAC AATGCACCAG 20

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:  
TCCACAGAGG GCTTCATCAC 20

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:  
CCTGACTGGC CTAAGCACAG 20

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:  
AAGCCTCATA ACCACCACTG 20

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:  
TGTCACGGT GACAAGTG 20

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TTGTACACCA GCTGCAGGTC

20

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GGGTGTGGTG CAGATGAGTC

20

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

ATCACACTCT TATAGCTCAG

20

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GTGGGAAGCT TTCCTCAGAC

20

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

TGATGAACAT GGCCTGGAG

20

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CATTGTGGAT GTACTACCAC

20

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

TGTGTTTTC AACCTGAGTG

20

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

ATAGTGGCAC CACTTACGAG

20

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

AATTCTGCAA CGTGATGGCG

20

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

CACAAGATGC CTCGCTGTG

20

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

AATCCGGACA AGGTACAGTC

20

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

GCACGAGTGG CACAAGCGTG

20

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GCAAGCGTGT GGTGTCAGTG

20

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

TGTTTGAACA GGCTCTGGAC

20

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

CGGCATGGCA ATGAGGACAC

20

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

AGGACGAGAT GGACCTCCAG

20

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

CCCTCTGTCC TCTAGCCAC

20

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

TCTTGAGGGG ACTGACTCTG

20

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

TGAGTGAGGA GGCAGATGTC

20

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

TGGCTTTGAA GAAAGAGCTG

20

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GCAAAAGACC AGGCTGACTG

20

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

TGCAGCTCCT TGGCTTCTC

20

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GATTCACAGT CCCAAGGCTC

20

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ATCTGGATGA GCGGTTGAG

20

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GGTCACTCTC CGACGAGGAG

20

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GGATCCAAAG TTCGTCTCTG

20

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CGCTGTGTGT CTGATCCCTC

20

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

ATGAAGGTAA ACCCCGGGAG

20

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

TGGTCTCTGG CTCTGAGCAC

20

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GCCTGGAGAA GCCCAGTCTG

20

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

CACACTCTGG ACCGTTGCTG

20

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

AAAGCTCCGC AGCCGAGTG

20

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

TCTTCCAGGA AGCTGCGGTC

20

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

GATGGTGGGG CAGCATTGAG

20



(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GTCACCAGTG GTGCTGCAG

20

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

ACCTCACGGT TGCCAACCTG

20

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

CGCAACAGCG TCTCCCTCG

20

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

AGTACCTTCA TAAGTTCTTC

20

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

TCCCAGACTT CAACCTTCAC

20

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

AAACATCTTC CCGGTCGGAC

20

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

GCTGAGCACC TTACCTCAC

20

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GACGTCCGTC CGGGAAGATG

20

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

ACACAGGAGA TGCAGGTCAC

20

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GAGTCTTCCA TGAAGAACAG

20

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GCAGTGAGGA AGGTAAGGAG

20

(2) INFORMATION FOR SEQ ID NO:147:

(D) TOPOLOGY. (linear)

(ix) FEATURE:

(D) OTHER INFORMATION:

CGGCTCAAAG	GAGCCGCCCCG	CGCAGAGGAG	ATTGGTGCTT	CGGAGCCCGCG	GCAGTGCGCC	60
CCGCTGAGCT	CGGCGCCGCTG	TGCGGGTGT	TGTGATGTGT	TCTGTATGGG	AGAGGAGGTA	120
GGAGGAGGAA	AGAGAAGCAA	GAGTTGTGCT	TCTGGGTCGG	TCTCCCCCGC	GCTCTACATG	180
TCCTCGCGAC	TGAAGAGAGC	GAAAGAGGAGC	CGTAGCGGCGC	CCCCCTCCGC	GCGCCGAGTA	240
TAGTCTCTCG	CAGCAGCGCC	TCTGGCGCTC	CCTTGGATCT	AGAGCCGCGAT	TCCGCCAAGT	300
TTTGGGAAAT	GGGAGATGAT	GACAGCTGCG	ACCTGAACCTA	ATGACTATTA	TAGGCAACAC	360
CATTCCAGAA	ATTTCAGG	ATT	AGG	GAT	ATC	410
	Met	Asn	Gly	Asp	Met	His
	Val	Pro	Arg	Val	Pro	Thr
	1	4	5	10		

ACT CTT GCG GGG ATT GCT AGT CTC ACA GAC CTC CTG AAC CAG CTG CCT 458  
Thr Leu Ala Gly Ile Ala Ser Leu Thr Asp Leu Leu Asn Gln Leu Pro  
15 20 25

CTT CCA TCT CCT TTA CCT GCT ACA ACT ACA AAG AGC CTT CTC TTT AAT 506  
Leu Pro Ser Pro Leu Pro Ala Thr Thr Lys Ser Leu Leu Phe Asn  
30 35 40

GCA CGA ATA GCA GAA GAG GTG AAC TGC CTT TTG GCT TGT AGG GAT GAC 554  
Ala Arg Ile Ala Glu Glu Val Asn Cys Leu Leu Ala Cys Arg Asp Asp  
45 50 55

AAT TTG GTT TCA CAG CTT GTC CAT AGC CTC AAC CAG GTA TCA ACA GAT 602  
Asn Leu Val Ser Gln Leu Val His Ser Leu Asn Gln Val Ser Thr Asp  
60 65 70 75

CAC ATA GAG TTG AAA GAT AAC CTT GGC AGT GAT GAC CCA GAA GGT GAC 650  
His Ile Glu Leu Lys Asp Asn Leu Gly Ser Asp Asp Pro Glu Gly Asp  
80 85 90

ATA CCA GTC TTG TTG CAG GCC GTC CTG GCA AGG AGT CCT AAT GTT TTC 698  
Ile Pro Val Leu Leu Gln Ala Val Leu Ala Arg Ser Pro Asn Val Phe  
95 100 105

AGG GAG AAA AGC ATG CAG AAC AGA TAT GTA CAA AGT GGA ATG ATG ATG 746  
Arg Glu Lys Ser Met Gln Asn Arg Tyr Val Gln Ser Gly Met Met Met  
110 115 120

TCT CAG TAT AAA CTT TCT CAG AAT TCC ATG CAC AGT AGT CCT GCA TCT 794  
Ser Gln Tyr Lys Leu Ser Gln Asn Ser Met His Ser Ser Pro Ala Ser  
125 130 135

TCC AAT TAT CAA CAA ACC ACT ATC TCA CAT AGC CCC TCC AGC CGG TTT 842  
Ser Asn Tyr Gln Gln Thr Thr Ile Ser His Ser Pro Ser Ser Arg Phe  
140 145 150 155

GTG CCA CCA CAG ACA AGC TCT GGG AAC AGA TTT ATG CCA CAG CAA AAT 890  
Val Pro Pro Gln Thr Ser Ser Gly Asn Arg Phe Met Pro Gln Gln Asn  
160 165 170

AGC CCA GTG CCT AGT CCA TAC GCC CCA CAA AGC CCT GCA GGA TAC ATG 938  
Ser Pro Val Pro Ser Pro Tyr Ala Pro Gln Ser Pro Ala Gly Tyr Met  
175 180 185

CCA TAT TCC CAT CCT TCA AGT TAC ACA ACA CAT CCA CAG ATG CAA CAA . 986  
Pro Tyr Ser His Pro Ser Ser Tyr Thr Thr His Pro Gln Met Gln Gln  
190 195 200

GCA TCG GTA TCA AGT CCC ATT GTT GCA GGT GGT TTG AGA AAC ATA CAT Ala Ser Val Ser Ser Pro Ile Val Ala Gly Gly Leu Arg Asn Ile His 205 210 215	1034
GAT AAT AAA GTT TCT GGT CCG TTG TCT GGC AAT TCA GCT AAT CAT CAT Asp Asn Lys Val Ser Gly Pro Leu Ser Gly Asn Ser Ala Asn His His 220 225 230 235	1082
GCT GAT AAT CCT AGA CAT GGT TCA AGT GAG GAC TAC CTA CAC ATG GTG Ala Asp Asn Pro Arg His Gly Ser Ser Glu Asp Tyr Leu His Met Val 240 245 250	1130
CAC AGG CTA AGT AGT GAC GAT GGA GAT TCT TCA ACA ATG AGG AAT GCT His Arg Leu Ser Ser Asp Asp Gly Asp Ser Ser Thr Met Arg Asn Ala 255 260 265	1178
GCA TCT TTT CCC TTG AGA TCT CCA CAG CCA GTA TGC TCC CCT GCT GGA Ala Ser Phe Pro Leu Arg Ser Pro Gln Pro Val Cys Ser Pro Ala Gly 270 275 280	1226
AGT GAA GGA ACT CCT AAA GGC TCA AGA CCA CCT TTA ATC CTA CAA TCT Ser Glu Gly Thr Pro Lys Gly Ser Arg Pro Pro Leu Ile Leu Gln Ser 285 290 295	1274
CAG TCT CTA CCT TGT TCA TCA CCT CGA GAT GTT CCA CCA GAT ATC TTG Gln Ser Leu Pro Cys Ser Ser Pro Arg Asp Val Pro Pro Asp Ile Leu 300 305 310 315	1322
CTA GAT TCT CCA GAA AGA AAA CAA AAG AAG CAG AAG AAA ATG AAA TTA Leu Asp Ser Pro Glu Arg Lys Gln Lys Lys Gln Lys Lys Met Tyr Lys Leu 320 325 330	1370
GGC AAG GAT GAA AAA GAG CAG AGT GAG AAA GCG GCA ATG TAT GAT ATA Gly Lys Asp Glu Lys Glu Gln Ser Glu Lys Ala Ala Met Tyr Asp Ile 335 340 345	1418
ATT AGT TCT CCA TCC AAG GAC TCT ACT AAA CTT ACA TTA AGA CTT TCT Ile Ser Ser Pro Ser Lys Asp Ser Thr Lys Leu Thr Leu Arg Leu Ser 350 355 360	1466
CGT GTA AGG TCT TCA GAC ATG GAC CAG CAA GAG GAT ATG ATT TCT GGT Arg Val Arg Ser Ser Asp Met Asp Gln Gln Glu Asp Met Ile Ser Gly 365 370 375	1514
GTG GAA AAT AGC AAT GTT TCA GAA AAT GAT ATT CCT TTT AAT GTG CAG Val Glu Asn Ser Asn Val Ser Glu Asn Asp Ile Pro Phe Asn Val Gln 380 385 390 395	1562
TAC CCA GGA CAG ACT TCA AAA ACA CCC ATT ACT CCA CAA GAT ATA AAC Tyr Pro Gly Gln Thr Ser Lys Thr Pro Ile Thr Pro Gln Asp Ile Asn 400 405 410	1610
CGC CCA CTA AAT GCT GCT CAA TGT TTG TCG CAG CAA GAA CAA ACA GCA Arg Pro Leu Asn Ala Ala Gln Cys Leu Ser Gln Gln Glu Gln Thr Ala 415 420 425	1658
TTC CTT CCA GCA AAT CAA GTG CCT GTT TTA CAA CAG AAC ACT TCA GTT Phe Leu Pro Ala Asn Gln Val Pro Val Leu Gln Gln Asn Thr Ser Val 430 435 440	1706
GCT GCA AAA CAA CCC CAG ACC AAT AGT CAC AAA ACC TTG GTG CAG CCT Ala Ala Lys Gln Pro Gln Thr Asn Ser His Lys Thr Leu Val Gln Pro 445 450 455	1754
GGA ACA GGC ATA GAG GTC TCA GCA GAG CTG CCC AAG GAC AAG ACC TAAGA Gly Thr Gly Ile Glu Val Ser Ala Glu Leu Pro Lys Asp Lys Thr 460 465 470	1804
TCCAGCAGGG AACTATGTAG TCACCCCGAG AGGCCAGCT CTCTCCGTGA GCTCTGGGCC TAGGGTGGGG GTGGTTGTTG GTTCTGCGCG CACTGTTCCT CCTACATGAT GGGTCCATCC CAGTTGGCTT CTCTCACTCG CTTCTCCCTG TGGAGAAGCC TGTCAGGTG TCACGTGCCTC CAGGAAGCTG TCTCTGATT CTCCAGTTGA ACAGTGAGAT TTGCCACCC TCACATGCAT CGCTCTGTGC CCTGGAATTG TAACCATAGG TTTTCTGTG TCCTGGAGGA CAAGGATGAG 1864 1924 1984 2044 2104	

GGCTTTCCAC TTGAGTCTCC CTGGTGGAGC CCAGCTCCTG ACATACCTGG TAAAAGTTCT 2164  
 CAAGAGAAGA ACATGGAGGA GGAATGTGGA TAACAACCTT GGCTGCCGTG GTGTTTCCAG 2224  
 CTAGGAAGAT GTAATGTCCC CACAACGGG GTAATGGCTT TGCTGCCGTG ACAGCTGTCT 2284  
 CAAGGCCAGG CCCTGGGCGC CAGCCCAAGC CCAAGGACTA GGTCCAGAGC CACACAGCGC 2344  
 CAGGCCACAT CGGCCTCACC TGGGACCTTT TGTGGGGTAC AGTCTCCGGC CCCACCCAGA 2404  
 CTTCTTGAAG GAGAGACCCC ATGGCAAGGA CTCAGCCACC TGCAGTTTCA TAAGCCCCCA 2464  
 GTGGGTTCCT AGGCATGAAG ACCACCGGTT AGAGGCTGAA CTGGCAGGAA CCTGTCTCCA 2524  
 GCCCTTCTCT ACCCCAGCCG GGCCTTGCTT CAGAGGCAGC ACCCAGGAGC TGGCCATGAC 2584  
 CCGTGGACTC CACTCAATCC CTCTTCTCCA GGAGCCATGC AAAGTGTGAG CCAGCCAGGC 2644  
 CCTGGGAAGG CAGTCATCAC CTCTTAAGGC ATTGTGGGTG TCGGTCTGCG AACTGCCAAG 2704  
 TGCAGCACAC GACCCGTGTC CGGTGTTTCA TAGCAGGAGG CCATGACCTG GCAACGATTG 2764  
 CACGCTCAAA GGGGCACCCG GGGGGCCCTG GGTGCGGCGG GATCAGCTTT CCCTGGGCAC 2824  
 ATCTGCCATC TTCCAGATCT CCAGGCTCTA TGTCTGTGAC AGGGAGGGAA GGCTCTGCC 2884  
 TGCCCTTCCG TCAGCTCTGC CAGTGCAGGC TGGGCAGCCT GGGCTTTAGA GCTGGCTTCT 2944  
 GCCCACACTT TCTCCGTGAA AGGAAACAA CTATGAGTCT GCCAACGCA TCTCAGATGC 3004  
 GTTTTAAAAA ATTCTGGTCC CCCTCTCTG TCCATCATC CCGCTCGGGG ACTTCTCTCT 3064  
 TCGGTGTTCT TACCCCATTA CTCTGTCACT GCCACATTTT CACCTGGGCG TGCCCTTTGT 3124  
 CTCACCTGAA AACTCCTGAA AATCTTGAA TGGATTTCTA GGTCACTGGG GACTCCGGCA 3184  
 CCAACATTCG CTTCAGAATA AAGGGCGCCC CGCGTCCCCC AGCAGCTTCC CAAGCCACAC 3244  
 GCGTAGCTTC CTTCCCTATC CTTGCAGCCT GAGGCTCCCT TCAGCCACCC TTAGTCTCCC 3304  
 ACCTGGGCTC CTGCCCCGCC CCTGGCTAGC AGCGCTTCT CCACCGGGG CCCCCTCTGT 3364  
 CACAGAGCCC CCTCAGCTCC CTGGGATGA GGGGCCAGGC CATGACCTG AAGTCTAGC 3424  
 CTTGGGCTTG ACCTCCAGG AGCGCCCTCC CCGCCCTCTC CCGGCCCGGG CCGCTCTC 3484  
 TGTGCTGAG CTCTGGGTG TGGCCCGCAG ACTGAGCTGC GCTTGGGGGT CCTGGCGGCC 3544  
 TGGGCGTCC CGCACCGAAC CAGGCGGTC GAGGCCGCGC GGGGAAGGCG GAGGTCTTCT 3604  
 TGGGGCTCC TCCGAGCCT GAGGCGGCTC CTTCGCCGCG GCGCCCGGG GTTCTGTGCG 3664  
 AGCCGGGGCC TCCGCTCTG GGTGACCGG TGAGACCCCG GGGGAGGCG CTGGGAGAGG 3724  
 GCGGCTCTG CTCCCGGGTC CCAACGCGC TGGCTGCCCC TCAGGAGGGA CGCGGACCTC 3784  
 CACCCAGGCG GCTGGGCGC GCAGCGCCG TCTTCCGCT CCGCGAGCCT GGACGCTTCC 3844  
 CGAGGCGCGC CGCGCGGGCC CCACGCGCGG CCCCATCCCG AGGCGAGGAC TGCCCTTCCC 3904  
 GAGCTGGCGG CCCCCAGCCT GGAGGAGCGG GCCCAGAGC CCGTCCAGC CCGCCAGC 3964  
 CCACTCTGAG CCGCGAGGCC CGGCTGGTCT CGAGTGGCGG TCTCTGGGCC CGGCTTTTCC 4024  
 CGGGGAAGGA AAGCAAAAG CTT 4047

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Met Asn Gly Asp Met Pro His Val Pro Ile Thr Thr Leu Ala Gly Ile  
 1 5 10 15  
 Ala Ser Leu Thr Asp Leu Leu Asn Gln Leu Pro Leu Pro Ser Pro Leu  
 20 25 30  
 Pro Ala Thr Thr Thr Lys Ser Leu Leu Phe Asn Ala Arg Ile Ala Glu  
 35 40 45  
 Glu Val Asn Cys Leu Leu Ala Cys Arg Asp Asp Asn Leu Val Ser Gln  
 50 55 60  
 Leu Val His Ser Leu Asn Gln Val Ser Thr Asp His Ile Glu Leu Lys  
 65 70 75 80  
 Asp Asn Leu Gly Ser Asp Asp Pro Glu Gly Asp Ile Pro Val Leu Leu  
 85 90 95  
 Gln Ala Val Leu Ala Arg Ser Pro Asn Val Phe Arg Glu Lys Ser Met  
 100 105 110  
 Gln Asn Arg Tyr Val Gln Ser Gly Met Met Met Ser Gln Tyr Lys Leu  
 115 120 125  
 Ser Gln Asn Ser Met His Ser Ser Pro Ala Ser Ser Asn Tyr Gln Gln  
 130 135 140  
 Thr Thr Ile Ser His Ser Pro Ser Ser Arg Phe Val Pro Pro Gln Thr  
 145 150 155 160  
 Ser Ser Gly Asn Arg Phe Met Pro Gln Gln Asn Ser Pro Val Pro Ser  
 165 170 175  
 Pro Tyr Ala Pro Gln Ser Pro Ala Gly Tyr Met Pro Tyr Ser His Pro  
 180 185 190  
 Ser Ser Tyr Thr Thr His Pro Gln Met Gln Gln Ala Ser Val Ser Ser  
 195 200 205

Pro Ile Val Ala Gly Gly Leu Arg Asn Ile His Asp Asn Lys Val Ser  
 210 215 220  
 Gly Pro Leu Ser Gly Asn Ser Ala Asn His His Ala Asp Asn Pro Arg  
 225 230 235 240  
 His Gly Ser Ser Glu Asp Tyr Leu His Met Val His Arg Leu Ser Ser  
 245 250 255  
 Asp Asp Gly Asp Ser Ser Thr Met Arg Asn Ala Ala Ser Phe Pro Leu  
 260 265 270  
 Arg Ser Pro Gln Pro Val Cys Ser Pro Ala Gly Ser Glu Gly Thr Pro  
 275 280 285  
 Lys Gly Ser Arg Pro Pro Leu Ile Leu Gln Ser Gln Ser Leu Pro Cys  
 290 295 300  
 Ser Ser Pro Arg Asp Val Pro Pro Asp Ile Leu Leu Asp Ser Pro Glu  
 305 310 315 320  
 Arg Lys Gln Lys Lys Gln Lys Lys Met Lys Leu Gly Lys Asp Glu Lys  
 325 330 335  
 Glu Gln Ser Glu Lys Ala Ala Met Tyr Asp Ile Ile Ser Ser Pro Ser  
 340 345 350  
 Lys Asp Ser Thr Lys Leu Thr Leu Arg Leu Ser Arg Val Arg Ser Ser  
 355 360 365  
 Asp Met Asp Gln Gln Glu Asp Met Ile Ser Gly Val Glu Asn Ser Asn  
 370 375 380  
 Val Ser Glu Asn Asp Ile Pro Phe Asn Val Gln Tyr Pro Gly Gln Thr  
 385 390 395 400  
 Ser Lys Thr Pro Ile Thr Pro Gln Asp Ile Asn Arg Pro Leu Asn Ala  
 405 410 415  
 Ala Gln Cys Leu Ser Gln Gln Glu Gln Thr Ala Phe Leu Pro Ala Asn  
 420 425 430  
 Gln Val Pro Val Leu Gln Gln Asn Thr Ser Val Ala Ala Lys Gln Pro  
 435 440 445  
 Gln Thr Asn Ser His Lys Thr Leu Val Gln Pro Gly Thr Gly Ile Glu  
 450 455 460  
 Val Ser Ala Glu Leu Pro Lys Asp Lys Thr  
 465 470

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 26...799
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

AAGCTTTTGG AATTCGGCAC GAGAT GCT ACA CAG GCT ATA TTT GAA ATA CTG	52
Ala Thr Gln Ala Ile Phe Glu Ile Leu	
1 5	
GAG AAA TCC TGG TTG CCC CAG AAT TGT ACA CTG GTT GAT ATG AAG ATY	100
Glu Lys Ser Trp Leu Pro Gln Asn Cys Thr Leu Val Asp Met Lys Ile	
10 15 20 25	
GAA TTT GGT GTT GAT GTA ACC ACC AAA GAA ATT GTT CTT GAT GAT GTT	148
Glu Phe Gly Val Asp Val Thr Thr Lys Glu Ile Val Leu Ala Asp Val	
30 35 40	
ATT GAC AAT GAT TCC TGG AGA CTC TGG CCA TCA GGA GAT CGA AGC CAA	196
Ile Asp Asn Asp Ser Trp Arg Leu Trp Pro Ser Gly Asp Arg Ser Gln	
45 50 55	
CAG AAA GAC AAA CAG TCT TAT CGG GAC CTC AAA GAA GTA ACT CCT GAA	244
Gln Lys Asp Lys Gln Ser Tyr Arg Asp Leu Lys Glu Val Thr Pro Glu	
60 65 70	
GGG CTC CAA ATG GTA AAG AAA AAC TTT GAG TGG GTT GCA GAG AGA GTA	292



GCTGCCCTTT GGAAGGTCA CCAACCTCCT GATGCTGAAG GGGAAAAACC AGGCTTCAT 2446  
 CGAGATGAAC ACGGAGGAGG CTGCCAATAC CATGGTGAAC TACTACACCT CGGTGACCCC 2506  
 TGTGCTGCCG GCCCAGCCCA TCTACATCCA GTTCTCCAAC CACAAGGAGC TGAAGACCGA 2566  
 CAGCTCTCCC AACCAGGCGC GGGCCAGGC GGCCTGCAG GCGGTGAAC CGGTCCAGTC 2626  
 GGGGAACCTG GCTTGGCTG CCTCGGCGG GGCCTGGAT GCAGGGATGG CGATGGCGGG 2686  
 GCAGAGCCCC GTGCTCAGGA TCATCGTGGG GAACCTCTTC TACCTGTGA CCCTGGATGT 2746  
 GCTGCACCCAG ATTTTCTCCA AGTTCGGCAC AGTGTGAAAG ATCATCACCT TCACCAAGAA 2806  
 CAACCACTTC CAGGCCCTGC TGCAGTAGGC GGACCCCGTG AGCGCCGAGC ACGCCAAGCT 2866  
 GTCGCTGGAG GGCAGAACCA TCTACAACGC CTGCTGCACG CTGCGCATCG ACTTTTCCAA 2926  
 GCTCACCAGC CTCACGTCA AGTACAACAA TGACAAGAGC CGTGACTACC TCGTGCCGAA 2986  
 TTCTTGGAT CC 2998

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Ala Thr Gln Ala Ile Phe Glu Ile Leu Glu Lys Ser Trp Leu Pro Gln  
 1 5 10 15  
 Asn Cys Thr Leu Val Asp Met Lys Ile Glu Phe Gly Val Asp Val Thr  
 20 25 30  
 Thr Lys Glu Ile Val Leu Ala Asp Val Ile Asp Asn Asp Ser Trp Arg  
 35 40 45  
 Leu Trp Pro Ser Gly Asp Arg Ser Gln Gln Lys Asp Lys Gln Ser Tyr  
 50 55 60  
 Arg Asp Leu Lys Glu Val Thr Pro Glu Gly Leu Gln Met Val Lys Lys  
 65 70 75 80  
 Asn Phe Glu Trp Val Ala Glu Arg Val Glu Leu Leu Lys Ser Glu  
 85 90 95  
 Ser Gln Cys Arg Val Val Leu Met Gly Ser Thr Ser Asp Leu Gly  
 100 105 110  
 His Cys Glu Lys Ile Lys Lys Ala Cys Gly Asn Phe Gly Ile Pro Cys  
 115 120 125  
 Glu Leu Arg Val Thr Ser Ala His Lys Gly Pro Asp Glu Thr Leu Arg  
 130 135 140  
 Ile Lys Ala Glu Tyr Glu Gly Asp Gly Ile Pro Thr Val Phe Val Ala  
 145 150 155 160  
 Val Ala Gly Arg Ser Asn Gly Leu Gly Pro Val Met Ser Gly Asn Thr  
 165 170 175  
 Ala Tyr Pro Val Ile Ser Cys Pro Pro Leu Thr Pro Asp Trp Gly Val  
 180 185 190  
 Gln Asp Val Trp Ser Ser Leu Arg Leu Pro Ser Gly Leu Cys Lys Ser  
 195 200 205  
 Thr Val Leu Ser Pro Glu Gly Ser Ala Gln Phe Ala Ala Gln Ile Phe  
 210 215 220  
 Gly Leu Ser Asn His Leu Val Trp Ser Lys Leu Arg Ala Ser Ile Leu  
 225 230 235 240  
 Asn Thr Trp Ile Ser Leu Lys Gln Ala Asp Lys Lys Ile Arg Glu Cys  
 245 250 255  
 Asn Leu

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1038 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Ile Gln Arg Phe Gly Thr Ser Gly His Ile Met Asn Leu Gln Ala Gln  
 1 5 10 15



Pro Lys Ala Gln Asn Lys Arg Lys Arg Cys Leu Phe Gly Gly Gln Glu  
 20 25 30  
 Pro Ala Pro Lys Glu Gln Pro Pro Leu Gln Pro Pro Gln Gln Ser  
 35 40 45  
 Ile Arg Val Lys Glu Glu Gln Tyr Leu Gly His Glu Gly Pro Gly Gly  
 50 55 60  
 Ala Val Ser Thr Ser Glu Pro Val Glu Leu Pro Pro Ser Ser Leu  
 65 70 75 80  
 Ala Leu Leu Asn Ser Val Val Tyr Gly Pro Glu Arg Thr Ser Ala Ala  
 85 90 95  
 Met Leu Ser Gln Gln Val Ala Ser Val Lys Trp Pro Asn Ser Val Met  
 100 105 110  
 Ala Pro Gly Arg Gly Pro Glu Arg Gly Gly Gly Gly Val Ser Asp  
 115 120 125  
 Ser Ser Trp Gln Gln Gln Pro Gly Gln Pro Pro His Ser Thr Trp  
 130 135 140  
 Asn Cys His Ser Leu Ser Leu Tyr Ser Ala Thr Lys Gly Ser Pro His  
 145 150 155 160  
 Pro Gly Val Gly Val Pro Thr Tyr Tyr Asn His Pro Glu Ala Leu Lys  
 165 170 175  
 Arg Glu Lys Ala Gly Gly Pro Gln Leu Asp Arg Tyr Val Arg Pro Met  
 180 185 190  
 Met Pro Gln Lys Val Gln Leu Glu Val Gly Arg Pro Gln Ala Pro Leu  
 195 200 205  
 Asn Ser Phe His Ala Ala Lys Lys Pro Pro Asn Gln Ser Leu Pro Leu  
 210 215 220  
 Gln Pro Phe Gln Leu Ala Phe Gly His Gln Val Asn Arg Gln Val Phe  
 225 230 235 240  
 Arg Gln Gly Pro Pro Pro Asn Pro Val Ala Ala Phe Pro Pro Gln  
 245 250 255  
 Lys Gln Gln Gln Gln Gln Gln Pro Gln Gln Gln Gln Gln Gln  
 260 265 270  
 Ala Ala Leu Pro Gln Met Pro Leu Phe Glu Asn Phe Tyr Ser Met Pro  
 275 280 285  
 Gln Gln Pro Ser Gln Gln Pro Gln Asp Phe Gly Leu Gln Pro Ala Gly  
 290 295 300  
 Pro Leu Gly Gln Ser His Leu Ala His His Ser Met Ala Pro Tyr Pro  
 305 310 315 320  
 Phe Pro Pro Asn Pro Asp Met Asn Pro Glu Leu Arg Lys Ala Leu Leu  
 325 330 335  
 Gln Asp Ser Ala Pro Gln Pro Ala Leu Pro Gln Val Gln Ile Pro Phe  
 340 345 350  
 Pro Arg Arg Ser Arg Arg Leu Ser Lys Glu Gly Ile Leu Pro Pro Ser  
 355 360 365  
 Ala Leu Asp Gly Ala Gly Thr Gln Pro Gly Gln Glu Ala Thr Gly Asn  
 370 375 380  
 Leu Phe Leu His His Trp Pro Leu Gln Gln Pro Pro Gly Ser Leu  
 385 390 395 400  
 Gly Gln Pro His Pro Glu Ala Leu Gly Phe Pro Leu Glu Leu Arg Glu  
 405 410 415  
 Ser Gln Leu Leu Pro Asp Gly Glu Arg Leu Ala Pro Asn Gly Arg Glu  
 420 425 430  
 Arg Glu Ala Pro Ala Met Gly Ser Glu Glu Gly Met Arg Ala Val Ser  
 435 440 445  
 Thr Gly Asp Cys Gly Gln Val Leu Arg Gly Gly Val Ile Gln Ser Thr  
 450 455 460  
 Arg Arg Arg Arg Ala Ser Gln Glu Ala Asn Leu Leu Thr Leu Ala  
 465 470 475 480  
 Gln Lys Ala Val Glu Leu Ala Ser Leu Gln Asn Ala Lys Asp Gly Ser  
 485 490 495  
 Gly Ser Glu Glu Lys Arg Lys Ser Val Leu Ala Ser Thr Lys Cys  
 500 505 510  
 Gly Val Glu Phe Ser Glu Pro Ser Leu Ala Thr Lys Arg Ala Arg Glu  
 515 520 525  
 Asp Ser Gly Met Val Pro Leu Ile Ile Pro Val Ser Val Pro Val Arg  
 530 535 540  
 Thr Val Asp Pro Thr Glu Ala Ala Gln Ala Gly Gly Leu Asp Glu Asp  
 545 550 555 560  
 Gly Lys Gly Leu Glu Gln Asn Pro Ala Glu His Lys Pro Ser Val Ile  
 565 570 575  
 Val Thr Arg Arg Ser Thr Arg Ile Pro Gly Thr Asp Ala Gln Ala  
 580 585 590  
 Gln Ala Glu Asp Met Asn Val Lys Leu Glu Gly Glu Pro Ser Val Arg

595                      600                      605  
 Lys Pro Lys Gln Arg Pro Arg Pro Glu Pro Leu Ile Ile Pro Thr Lys  
 610                      615                      620  
 Ala Gly Thr Phe Ile Ala Pro Pro Val Tyr Ser Asn Ile Thr Pro Tyr  
 625                      630                      635                      640  
 Gln Ser His Leu Arg Ser Pro Val Arg Leu Ala Asp His Pro Ser Glu  
 645                      650                      655  
 Arg Ser Phe Glu Leu Pro Pro Tyr Thr Pro Pro Ile Leu Ser Pro  
 660                      665                      670  
 Val Arg Glu Gly Ser Gly Leu Tyr Phe Asn Ala Ile Ile Ser Thr Ser  
 675                      680                      685  
 Thr Ile Pro Ala Pro Pro Ile Thr Pro Lys Ser Ala His Arg Thr  
 690                      695                      700  
 Leu Leu Arg Thr Asn Ser Ala Glu Val Thr Pro Pro Val Leu Ser Val  
 705                      710                      715                      720  
 Met Gly Glu Ala Thr Pro Val Ser Ile Glu Pro Arg Ile Asn Val Gly  
 725                      730                      735  
 Ser Arg Phe Gln Ala Glu Ile Pro Leu Met Arg Asp Arg Ala Leu Ala  
 740                      745                      750  
 Ala Ala Asp Pro His Lys Ala Asp Leu Val Trp Gln Pro Trp Glu Asp  
 755                      760                      765  
 Leu Glu Ser Ser Arg Glu Lys Gln Arg Gln Val Glu Asp Leu Leu Thr  
 770                      775                      780  
 Ala Ala Cys Ser Ser Ile Phe Pro Gly Ala Gly Thr Asn Gln Glu Leu  
 785                      790                      795                      800  
 Ala Leu His Cys Leu His Glu Ser Arg Gly Asp Ile Leu Glu Thr Leu  
 805                      810                      815  
 Asn Lys Leu Leu Leu Lys Lys Pro Leu Arg Pro His Asn His Pro Leu  
 820                      825                      830  
 Ala Thr Tyr His Tyr Thr Gly Ser Asp Gln Trp Lys Met Ala Glu Arg  
 835                      840                      845  
 Lys Leu Phe Asn Lys Gly Ile Ala Ile Tyr Lys Lys Asp Phe Phe Leu  
 850                      855                      860  
 Val Gln Lys Leu Ile Gln Thr Lys Thr Val Ala Gln Cys Val Glu Phe  
 865                      870                      875                      880  
 Tyr Tyr Thr Tyr Lys Lys Gln Val Lys Ile Gly Arg Asn Gly Thr Leu  
 885                      890                      895  
 Thr Phe Gly Asp Val Asp Thr Ser Asp Glu Lys Ser Ala Gln Glu Glu  
 900                      905                      910  
 Val Glu Val Asp Ile Lys Thr Ser Gln Lys Phe Pro Arg Val Pro Leu  
 915                      920                      925  
 Pro Arg Arg Glu Ser Pro Ser Glu Glu Arg Leu Glu Pro Lys Arg Glu  
 930                      935                      940  
 Val Lys Glu Pro Arg Lys Glu Gly Glu Glu Glu Val Pro Glu Ile Gln  
 945                      950                      955                      960  
 Glu Lys Glu Glu Gln Glu Glu Gly Arg Glu Arg Ser Arg Arg Ala Ala  
 965                      970                      975  
 Ala Val Lys Ala Thr Gln Thr Leu Gln Ala Asn Glu Ser Ala Ser Asp  
 980                      985                      990  
 Ile Leu Ile Leu Arg Ser His Glu Ser Asn Ala Pro Gly Ser Ala Gly  
 995                      1000                      1005  
 Gly Gln Ala Ser Glu Lys Pro Arg Glu Gly Thr Gly Lys Ser Arg Arg  
 1010                      1015                      1020  
 Ala Leu Pro Phe Ser Glu Lys Lys Lys Lys Lys Lys Ala  
 1025                      1030                      1035

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Ile Arg His Glu Val Ser Phe Leu Trp Asn Thr Glu Ala Ala Cys Pro  
 1                      5                      10                      15  
 Ile Gln Thr Thr Thr Asp Thr Asp Gln Ala Cys Ser Ile Arg Asp Pro  
 20                      25                      30  
 Asn Ser Gly Phe Val Phe Asn Leu Asn Pro Leu Asn Ser Ser Gln Gly  
 35                      40                      45

Tyr Asn Val Ser Gly Ile Gly Lys Ile Phe Met Phe Asn Val Cys Gly  
 50 55 60  
 Thr Met Pro Val Cys Gly Thr Ile Leu Gly Lys Pro Ala Ser Gly Cys  
 65 70 75 80  
 Glu Ala Glu Thr Gln Thr Glu Glu Leu Lys Asn Trp Lys Pro Ala Arg  
 85 90 95  
 Pro Val Gly Ile Glu Lys Ser Leu Gln Leu Ser Thr Glu Gly Phe Ile  
 100 105 110  
 Thr Leu Thr Tyr Lys Gly Pro Leu Ser Ala Lys Gly Thr Ala Asp Ala  
 115 120 125  
 Phe Ile Val Arg Phe Val Cys Asn Asp Asp Val Tyr Ser Gly Pro Leu  
 130 135 140  
 Lys Phe Leu His Gln Asp Ile Asp Ser Gly Gln Gly Ile Arg Asn Thr  
 145 150 155 160  
 Tyr Phe Glu Phe Glu Thr Ala Leu Ala Cys Val Pro Ser Pro Val Asp  
 165 170 175  
 Cys Gln Val Thr Asp Leu Ala Gly Asn Glu Tyr Asp Leu Thr Gly Leu  
 180 185 190  
 Ser Thr Val Arg Lys Pro Trp Thr Ala Val Asp Thr Ser Val Asp Gly  
 195 200 205  
 Arg Lys Arg Thr Phe Tyr Leu Ser Val Cys Asn Pro Leu Pro Tyr Ile  
 210 215 220  
 Pro Gly Cys Gln Gly Ser Ala Val Gly Ser Cys Leu Val Ser Glu Gly  
 225 230 235 240  
 Asn Ser Trp Asn Leu Gly Val Val Gln Met Ser Pro Gln Ala Ala Ala  
 245 250 255  
 Asn Gly Ser Leu Ser Ile Met Tyr Val Asn Gly Asp Lys Cys Gly Asn  
 260 265 270  
 Gln Arg Phe Ser Thr Arg Ile Thr Phe Glu Cys Ala Gln Ile Ser Gly  
 275 280 285  
 Ser Pro Ala Phe Gln Leu Gln Asp Gly Cys Glu Tyr Val Phe Ile Trp  
 290 295 300  
 Arg Thr Val Glu Ala Cys Pro Val Val Arg Val Glu Gly Asp Asn Cys  
 305 310 315 320  
 Glu Val Lys Asp Pro Arg His Gly Asn Leu Tyr Asp Leu Lys Pro Leu  
 325 330 335  
 Gly Leu Asn Asp Thr Ile Val Ser Ala Gly Glu Tyr Thr Tyr Phe  
 340 345 350  
 Arg Val Cys Gly Lys Leu Ser Ser Asp Val Cys Pro Thr Ser Asp Lys  
 355 360 365  
 Ser Lys Val Val Ser Ser Cys Gln Glu Lys Arg Glu Pro Gln Gly Phe  
 370 375 380  
 His Lys Val Ala Gly Leu Thr Gln Lys Leu Thr Tyr Glu Asn Gly  
 385 390 395 400  
 Leu Leu Lys Met Asn Phe Thr Gly Gly Asp Thr Cys His Lys Val Tyr  
 405 410 415  
 Gln Arg Ser Thr Ala Ile Phe Phe Tyr Cys Asp Arg Gly Thr Gln Arg  
 420 425 430  
 Pro Val Phe Leu Lys Glu Thr Ser Asp Cys Ser Tyr Leu Phe Glu Trp  
 435 440 445  
 Arg Thr Gln Tyr Ala Cys Pro Phe Asp Leu Thr Glu Cys Ser Phe  
 450 455 460  
 Lys Asp Gly Ala Gly Asn Ser Phe Asp Leu Ser Ser Leu Ser Arg Tyr  
 465 470 475 480  
 Ser Asp Asn Trp Glu Ala Ile Thr Gly Thr Gly Asp Pro Glu His Tyr  
 485 490 495  
 Leu Ile Asn Val Cys Lys Ser Leu Ala Pro Gln Ala Gly Thr Glu Pro  
 500 505 510  
 Cys Pro Pro Glu Ala Ala Ala Cys Leu Leu Gly Gly Ser Lys Pro Val  
 515 520 525  
 Asn Leu Gly Arg Val Arg Asp Gly Pro Gln Trp Arg Asp Gly Ile Ile  
 530 535 540  
 Val Leu Lys Tyr Val Asp Gly Asp Leu Cys Pro Asp Gly Ile Arg Lys  
 545 550 555 560  
 Lys Ser Thr Thr Ile Arg Phe Thr Cys Ser Glu Ser Gln Val Asn Ser  
 565 570 575  
 Arg Pro Met Phe Ile Ser Ala Val Glu Asp Cys Glu Tyr Thr Phe Ala  
 580 585 590  
 Trp Pro Thr Ala Thr Ala Cys Pro Met Lys Ser Asn Glu His Asp Asp  
 595 600 605  
 Cys Gln Val Thr Asn Pro Ser Thr Gly His Leu Phe Asp Leu Ser Ser  
 610 615 620  
 Leu Ser Gly Arg Ala Gly Phe Thr Ala Ala Tyr Ser Glu Lys Gly Leu

625                      630                      635                      640  
 Val Tyr Met Ser Ile Cys Gly Glu Asn Glu Asn Cys Pro Pro Gly Val  
                                  645                      650                      655  
 Gly Ala Cys Phe Gly Gln Thr Arg Ile Ser Val Gly Lys Ala Asn Lys  
                                  660                      665                      670  
 Arg Leu Arg Tyr Val Asp Gln Val Leu Gln Leu Val Tyr Lys Asp Gly  
                                  675                      680                      685  
 Ser Pro Cys Pro Ser Lys Ser Gly Leu Ser Tyr Lys Ser Val Ile Ser  
                                  690                      695                      700  
 Phe Val Cys Arg Pro Glu Ala Gly Pro Thr Asn Arg Pro Met Leu Ile  
 705                      710                      715                      720  
 Ser Leu Asp Lys Gln Thr Cys Thr Leu Phe Phe Ser Trp His Thr Pro  
                                  725                      730                      735  
 Leu Ala Cys Glu Gln Ala Thr Glu Cys Ser Val Arg Asn Gly Ser Ser  
                                  740                      745                      750  
 Ile Val Asp Leu Ser Pro Leu Ile His Arg Thr Gly Gly Tyr Glu Ala  
                                  755                      760                      765  
 Tyr Asp Glu Ser Glu Asp Asp Ala Ser Asp Thr Asn Pro Asp Phe Tyr  
                                  770                      775                      780  
 Ile Asn Ile Cys Gln Pro Leu Asn Pro Met His Gly Val Pro Cys Pro  
 785                      790                      795                      800  
 Ala Gly Ala Ala Val Cys Lys Val Pro Ile Asp Gly Pro Pro Ile Asp  
                                  805                      810                      815  
 Ile Gly Arg Val Ala Gly Pro Pro Ile Leu Asn Pro Ile Ala Asn Glu  
                                  820                      825                      830  
 Ile Tyr Leu Asn Phe Glu Ser Ser Thr Pro Cys Gln Glu Phe Ser Cys  
                                  835                      840                      845  
 Lys

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 852 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Met Ala Arg Leu Ser Arg Pro Glu Arg Pro Asp Leu Val Phe Glu Glu  
 1                      5                      10                      15  
 Glu Asp Leu Pro Tyr Glu Glu Glu Ile Met Arg Asn Gln Phe Ser Val  
                                  20                      25                      30  
 Lys Cys Trp Leu His Tyr Ile Glu Phe Lys Gln Gly Ala Pro Lys Pro  
                                  35                      40                      45  
 Arg Leu Asn Gln Leu Tyr Glu Arg Ala Leu Lys Leu Leu Pro Cys Ser  
                                  50                      55                      60  
 Tyr Lys Leu Trp Tyr Arg Tyr Leu Lys Ala Arg Arg Ala Gln Val Lys  
                                  65                      70                      75                      80  
 His Arg Cys Val Thr Asp Pro Ala Tyr Glu Asp Val Asn Asn Cys His  
                                  85                      90                      95  
 Glu Arg Ala Phe Val Phe Met His Lys Met Pro Arg Leu Trp Leu Asp  
                                  100                      105                      110  
 Tyr Cys Gln Phe Leu Met Asp Gln Gly Arg Val Thr His Thr Arg Arg  
                                  115                      120                      125  
 Thr Phe Asp Arg Ala Leu Arg Ala Leu Pro Ile Thr Gln His Ser Arg  
                                  130                      135                      140  
 Ile Trp Pro Leu Tyr Leu Arg Phe Leu Arg Ser His Pro Leu Pro Glu  
                                  145                      150                      155                      160  
 Thr Ala Val Arg Gly Tyr Arg Arg Phe Leu Lys Leu Ser Pro Glu Ser  
                                  165                      170                      175  
 Ala Glu Glu Tyr Ile Glu Tyr Leu Lys Ser Ser Asp Arg Leu Asp Glu  
                                  180                      185                      190  
 Ala Ala Gln Arg Leu Ala Thr Val Val Asn Asp Glu Arg Phe Val Ser  
                                  195                      200                      205  
 Lys Ala Gly Lys Ser Asn Tyr Gln Leu Trp His Glu Leu Cys Asp Leu  
                                  210                      215                      220  
 Ile Ser Gln Asn Pro Asp Lys Val Gln Ser Leu Asn Val Asp Ala Ile  
                                  225                      230                      235                      240  
 Ile Arg Gly Gly Leu Thr Arg Phe Thr Asp Gln Leu Gly Lys Leu Trp  
                                  245                      250                      255

Cys Ser Leu Ala Asp Tyr Tyr Ile Arg Ser Gly His Phe Glu Lys Ala  
 260 265 270  
 Arg Asp Val Tyr Glu Glu Ala Ile Arg Thr Val Met Thr Val Arg Asp  
 275 280 285  
 Phe Thr Gln Val Phe Asp Ser Tyr Ala Gln Phe Glu Glu Ser Met Ile  
 290 295 300  
 Ala Ala Lys Met Glu Thr Ala Ser Glu Leu Gly Arg Glu Glu Glu Asp  
 305 310 315 320  
 Asp Val Asp Leu Glu Leu Arg Leu Ala Arg Phe Glu Gln Leu Ile Ser  
 325 330 335  
 Arg Arg Pro Leu Leu Leu Asn Ser Val Leu Leu Arg Gln Asn Pro His  
 340 345 350  
 His Val His Glu Trp His Lys Arg Val Ala Leu His Gln Gly Arg Pro  
 355 360 365  
 Arg Glu Ile Ile Asn Thr Tyr Thr Glu Ala Val Gln Thr Val Asp Pro  
 370 375 380  
 Phe Lys Ala Thr Gly Lys Pro His Thr Leu Trp Val Ala Phe Ala Lys  
 385 390 395 400  
 Phe Tyr Glu Asp Asn Gly Gln Leu Asp Asp Ala Arg Val Ile Leu Glu  
 405 410 415  
 Lys Ala Thr Lys Val Asn Phe Lys Gln Val Asp Asp Leu Ala Ser Val  
 420 425 430  
 Trp Cys Gln Cys Gly Glu Leu Glu Leu Arg His Glu Asn Tyr Asp Glu  
 435 440 445  
 Ala Leu Arg Leu Leu Arg Lys Ala Thr Ala Leu Pro Ala Arg Arg Ala  
 450 455 460  
 Glu Tyr Phe Asp Gly Ser Glu Pro Val Gln Asn Arg Val Tyr Lys Ser  
 465 470 475 480  
 Leu Lys Val Trp Ser Met Leu Ala Asp Leu Glu Glu Ser Leu Gly Thr  
 485 490 495  
 Phe Gln Ser Thr Lys Ala Val Tyr Asp Arg Ile Leu Asp Leu Arg Ile  
 500 505 510  
 Ala Thr Pro Gln Ile Val Ile Asn Tyr Ala Met Phe Leu Glu Glu His  
 515 520 525  
 Lys Tyr Phe Glu Glu Ser Phe Lys Ala Tyr Glu Arg Gly Ile Ser Leu  
 530 535 540  
 Phe Lys Trp Pro Asn Val Ser Asp Ile Trp Ser Thr Tyr Leu Thr Lys  
 545 550 555 560  
 Phe Ile Ala Arg Tyr Gly Gly Arg Lys Leu Glu Arg Ala Arg Asp Leu  
 565 570 575  
 Phe Glu Gln Ala Leu Asp Gly Cys Pro Pro Lys Tyr Ala Lys Thr Leu  
 580 585 590  
 Tyr Leu Leu Tyr Ala Gln Leu Glu Glu Glu Trp Gly Leu Ala Arg His  
 595 600 605  
 Ala Met Ala Val Tyr Glu Arg Ala Thr Arg Ala Val Glu Pro Ala Gln  
 610 615 620  
 Gln Tyr Asp Met Phe Asn Ile Tyr Ile Lys Arg Ala Ala Glu Ile Tyr  
 625 630 635 640  
 Gly Val Thr His Thr Arg Gly Ile Tyr Gln Lys Ala Ile Glu Val Leu  
 645 650 655  
 Ser Asp Glu His Ala Arg Glu Met Cys Leu Arg Phe Ala Asp Met Glu  
 660 665 670  
 Cys Lys Leu Gly Glu Ile Asp Arg Ala Arg Ala Ile Tyr Ser Phe Cys  
 675 680 685  
 Ser Gln Ile Cys Asp Pro Arg Thr Thr Gly Ala Phe Trp Gln Thr Trp  
 690 695 700  
 Lys Asp Phe Glu Val Arg His Gly Asn Glu Asp Thr Ile Lys Glu Met  
 705 710 715 720  
 Leu Arg Ile Arg Arg Ser Val Gln Ala Thr Tyr Asn Thr Gln Val Asn  
 725 730 735  
 Phe Met Ala Ser Gln Met Leu Lys Val Ser Gly Ser Ala Thr Gly Thr  
 740 745 750  
 Val Ser Asp Leu Ala Pro Gly Gln Ser Gly Met Asp Asp Met Lys Leu  
 755 760 765  
 Leu Glu Gln Arg Ala Glu Gln Leu Ala Ala Glu Ala Glu Arg Asp Gln  
 770 775 780  
 Pro Leu Arg Ala Gln Ser Lys Ile Leu Phe Val Arg Ser Asp Ala Ser  
 785 790 795 800  
 Arg Glu Glu Leu Ala Glu Leu Ala Gln Gln Val Asn Pro Glu Glu Ile  
 805 810 815  
 Gln Leu Gly Glu Asp Glu Asp Glu Asp Glu Met Asp Leu Glu Pro Asn  
 820 825 830  
 Glu Val Arg Leu Glu Gln Gln Ser Val Pro Ala Ala Val Phe Gly Ser

835  
Leu Lys Glu Asp  
850

840

845

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Met	Phe	Ser	Ala	Leu	Lys	Lys	Leu	Val	Gly	Ser	Asp	Gln	Ala	Pro	Gly
1				5				10					15		
Arg	Asp	Lys	Asn	Ile	Pro	Ala	Gly	Leu	Gln	Ser	Met	Asn	Gln	Ala	Leu
			20					25					30		
Gln	Arg	Arg	Phe	Ala	Lys	Gly	Val	Gln	Tyr	Asn	Met	Lys	Ile	Val	Ile
			35				40					45			
Arg	Gly	Asp	Arg	Asn	Thr	Gly	Lys	Thr	Ala	Leu	Trp	His	Arg	Leu	Gln
			50				55				60				
Gly	Arg	Pro	Phe	Val	Glu	Glu	Tyr	Ile	Pro	Thr	Gln	Glu	Ile	Gln	Val
			65				70				75			80	
Thr	Ser	Ile	His	Trp	Ser	Tyr	Lys	Thr	Thr	Asp	Asp	Ile	Val	Lys	Val
			85					90				95			
Glu	Val	Trp	Asp	Val	Val	Asp	Lys	Gly	Lys	Cys	Lys	Lys	Arg	Gly	Asp
			100					105				110			
Gly	Leu	Lys	Met	Glu	Asn	Asp	Pro	Gln	Glu	Xaa	Glu	Ser	Glu	Met	Ala
			115				120				125				
Leu	Asp	Ala	Glu	Phe	Leu	Asp	Val	Tyr	Lys	Asn	Cys	Asn	Gly	Val	Val
			130				135				140				
Met	Met	Phe	Asp	Ile	Thr	Lys	Gln	Trp	Thr	Phe	Asn	Tyr	Ile	Leu	Arg
			145				150				155			160	
Glu	Leu	Pro	Lys	Val	Pro	Thr	His	Val	Pro	Val	Cys	Val	Leu	Gly	Asn
			165					170				175			
Tyr	Arg	Asp	Met	Gly	Glu	His	Arg	Val	Ile	Leu	Pro	Asp	Asp	Val	Arg
			180				185					190			
Asp	Phe	Ile	Asp	Asn	Leu	Asp	Arg	Pro	Pro	Gly	Ser	Ser	Tyr	Phe	Arg
			195				200					205			
Tyr	Ala	Glu	Ser	Ser	Met	Lys	Asn	Ser	Phe	Gly	Leu	Lys	Tyr	Leu	His
			210				215				220				
Lys	Phe	Phe	Asn	Ile	Pro	Phe	Leu	Gln	Leu	Gln	Arg	Glu	Thr	Leu	Leu
			225				230				235			240	
Arg	Gln	Leu	Glu	Thr	Asn	Gln	Leu	Asp	Met	Asp	Ala	Thr	Leu	Glu	Glu
			245					250				255			
Leu	Ser	Val	Gln	Gln	Glu	Thr	Glu	Asp	Gln	Asn	Tyr	Gly	Ile	Phe	Leu
			260				265					270			
Glu	Met	Met	Glu	Ala	Arg	Ser	Arg	Gly	His	Ala	Ser	Pro	Leu	Ala	Ala
			275				280					285			
Asn	Gly	Gln	Ser	Pro	Ser	Pro	Gly	Ser	Gln	Ser	Pro	Val	Leu	Pro	Ala
			290				295					300			
Pro	Ala	Val	Ser	Thr	Gly	Ser	Ser	Ser	Pro	Gly	Thr	Pro	Gln	Pro	Ala
			305				310				315			320	
Pro	Gln	Leu	Pro	Leu	Asn	Ala	Ala	Pro	Pro	Ser	Ser	Val	Pro	Pro	Val
			325					330				335			
Pro	Pro	Ser	Glu	Ala	Leu	Pro	Pro	Pro	Ala	Cys	Pro	Ser	Ala	Pro	Ala
			340				345					350			
Pro	Arg	Arg	Ser	Ile	Ile	Ser	Arg	Leu	Phe	Gly	Thr	Ser	Pro	Ala	Thr
			355				360					365			
Glu	Ala	Ala	Pro	Pro	Pro	Pro	Glu	Pro	Val	Pro	Ala	Ala	Gln	Gly	Pro
			370				375					380			
Ala	Thr	Val	Gln	Ser	Val	Glu	Asp	Phe	Val	Pro	Asp	Asp	Arg	Leu	Asp
			385				390				395			400	
Arg	Ser	Phe	Leu	Glu	Asp	Thr	Thr	Pro	Ala	Arg	Asp	Glu	Lys	Lys	Val
			405					410				415			
Gly	Ala	Lys	Ala	Ala	Gln	Gln	Asp	Ser	Asp	Ser	Asp	Gly	Glu	Ala	Leu
			420				425					430			
Gly	Gly	Asn	Pro	Met	Val	Ala	Gly	Phe	Gln	Asp	Asp	Val	Asp	Leu	Glu
			435				440					445			
Asp	Gln	Pro	Arg	Gly	Ser	Pro	Pro	Leu	Pro	Ala	Gly	Pro	Val	Pro	Ser
			450				455					460			

Gln Asp Ile Thr Leu Ser Ser Glu Glu Glu Ala Glu Val Ala Ala Pro  
 465 470 475 480  
 Thr Lys Gly Pro Ala Pro Ala Pro Gln Gln Cys Ser Glu Pro Glu Thr  
 485 490 495  
 Lys Trp Ser Ser Ile Pro Ala Ser Lys Pro Arg Arg Gly Thr Ala Pro  
 500 505 510  
 Thr Arg Thr Ala Ala Pro Pro Trp Pro Gly Gly Val Ser Val Arg Thr  
 515 520 525  
 Gly Pro Glu Lys Arg Ser Ser Thr Arg Pro Pro Ala Glu Met Glu Pro  
 530 535 540  
 Gly Lys Gly Glu Gln Ala Ser Ser Ser Glu Ser Asp Pro Glu Gly Pro  
 545 550 555 560  
 Ile Ala Ala Gln Met Leu Ser Phe Val Met Asp Asp Pro Asp Phe Glu  
 565 570 575  
 Ser Glu Gly Ser Asp Thr Gln Arg Arg Ala Asp Asp Phe Pro Val Arg  
 580 585 590  
 Asp Asp Pro Ser Asp Val Thr Asp Glu Asp Glu Gly Pro Ala Glu Pro  
 595 600 605  
 Pro Pro Pro Pro Lys Leu Pro Leu Pro Ala Phe Arg Leu Lys Asn Asp  
 610 615 620  
 Ser Asp Leu Phe Gly Leu Gly Leu Glu Glu Ala Gly Pro Lys Glu Ser  
 625 630 635 640  
 Ser Glu Glu Gly Lys Glu Gly Lys Thr Pro Ser Lys Glu Lys Lys  
 645 650 655  
 Lys Thr Lys Ser Phe Ser Arg Val Leu Leu Glu Arg Pro Arg Ala His  
 660 665 670  
 Arg Phe Ser Thr Arg Val Gly Tyr Gln Val Ser Val Pro Asn Ser Pro  
 675 680 685  
 Tyr Ser Glu Ser Tyr  
 690